GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:54:16 ; Search time 83 Seconds
(without alignments)
47.167 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

size : 0

Total number of hits satisfying chosen parameters: 5709

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5 | 26.3 | 14 | 11 | Q9Z0G5 | Q9z0g5 mus musculu |
| 2 | 4 | 21.1 | 17 | 4 | Q16310 | Q16310 homo sapien |
| 3 | 4 | 21.1 | 17 | 4 | Q13376 | Q13376 homo sapien |
| 4 | 4 | 21.1 | 19 | 4 | Q16271 | Q16271 homo sapien |
| 5 | 4 | 21.1 | 20 | 11 | Q9QUZ1 | Q9quz1 rattus sp. |
| 6 | 3 | 15.8 | 10 | 2 | P83067 | P83067 bacillus ce |
| 7 | 3 | 15.8 | 10 | 2 | Q8RSU1 | Q8rsu1 helicobacte |
| 8 | 3 | 15.8 | 10 | 10 | P82937 | P82937 hordeum vul |
| 9 | 3 | 15.8 | 10 | 11 | Q9QVF7 | Q9qvf7 rattus sp. |
| 10 | 3 | 15.8 | 10 | 11 | Q9QVE8 | Q9qve8 mus sp. pro |
| 11 | 3 | 15.8 | 10 | 11 | Q9QVE7 | Q9qve7 mus sp. pro |
| 12 | 3 | 15.8 | 11 | 3 | Q9UR95 | Q9ur95 pichia angu |
| 13 | 3 | 15.8 | 11 | 4 | O60614 | O60614 homo sapien |
| 14 | 3 | 15.8 | 11 | 4 | Q9NY38 | Q9ny38 homo sapien |
| 15 | 3 | 15.8 | 11 | 5 | P83321 | P83321 penaeus mon |
| 16 | 3 | 15.8 | 11 | 5 | Q9VN99 | Q9vn99 drosophila |
| 17 | 3 | 15.8 | 11 | 5 | P82698 | P82698 leucophaea |
| 18 | 3 | 15.8 | 11 | 6 | Q9TRW5 | Q9trw5 bos taurus |
| 19 | 3 | 15.8 | 11 | 10 | Q04131 | Q04131 lycopersico |
| 20 | 3 | 15.8 | 11 | 11 | Q99N81 | Q99n81 mus musculu |
| 21 | 3 | 15.8 | 11 | 11 | Q9Z1H5 | Q9z1h5 mus musculu |
| 22 | 3 | 15.8 | 11 | 12 | Q89616 | Q89616 avian infec |
| 23 | 3 | 15.8 | 11 | 15 | Q9DZ32 | Q9dz32 human immun |
| 24 | 3 | 15.8 | 11 | 16 | Q9K7A4 | Q9k7a4 bacillus ha |
| 25 | 3 | 15.8 | 12 | 2 | O50303 | O50303 bacillus st |
| 26 | 3 | 15.8 | 12 | 2 | Q9R5F7 | Q9r5f7 helicobacte |
| 27 | 3 | 15.8 | 12 | 2 | Q9R5F5 | Q9r5f5 helicobacte |
| 28 | 3 | 15.8 | 12 | 6 | Q9TRT8 | Q9trt8 bos taurus |
| 29 | 3 | 15.8 | 12 | 6 | Q9XS31 | Q9xs31 sus scrofa |
| 30 | 3 | 15.8 | 12 | 10 | Q8SAS2 | Q8sas2 pinus sylve |
| 31 | 3 | 15.8 | 12 | 11 | Q9QZD0 | Q9qzd0 mus musculu |
| 32 | 3 | 15.8 | 12 | 11 | Q61331 | Q61331 mus musculu |
| 33 | 3 | 15.8 | 12 | 12 | Q69232 | Q69232 bovine herp |
| 34 | 3 | 15.8 | 13 | 2 | Q55234 | Q55234 synechocyst |
| 35 | 3 | 15.8 | 13 | 2 | Q47693 | Q47693 escherichia |
| 36 | 3 | 15.8 | 13 | 4 | Q9UM46 | Q9um46 homo sapien |
| 37 | 3 | 15.8 | 13 | 7 | Q29823 | Q29823 homo sapien |
| 38 | 3 | 15.8 | 13 | 8 | Q9XLI2 | Q9xli2 bemisia tab |
| 39 | 3 | 15.8 | 13 | 8 | Q9T2U1 | Q9t2ul bos taurus |
| 40 | 3 | 15.8 | 13 | 12 | Q9WMG5 | Q9wmg5 sigma virus |
| 41 | 3 | 15.8 | 14 | 2 | Q9R8P6 | Q9r8p6 chlamydia t |
| 42 | 3 | 15.8 | 14 | 2 | Q9R8P2 | Q9r8p2 chlamydia t |
| 43 | 3 | 15.8 | 14 | 2 | Q9R8N9 | Q9r8n9 chlamydia t |
| 44 | 3 | 15.8 | 14 | 2 | Q9R8N6 | Q9r8n6 chlamydia t |
| 45 | 3 | 15.8 | 14 | 2 | Q9R8N2 | Q9r8n2 chlamydia t |

ALIGNMENTS

RESULT 1
Q9Z0G5
ID Q9Z0G5 PRELIMINARY; PRT; 14 AA.
AC Q9Z0G5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SHORTER isoform of interleukin 15 (Fragment).
GN IL15 OR INTERLEUKIN 15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALBC;
RA Nishimura H.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALBC;
RX MEDLINE=98211658; PubMed=9551932;
RA Nishimura H., Washizu J., Nakamura N., Enomoto A., Yoshikai Y.;
RT "Translational efficiency is up-regulated by alternative exon in
RT murine IL-15 mRNA.";
RL J. Immunol. 160:936-942(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Prinz M., Hanisch U.K., Kettenmann H., Kirchhoff F.;
RT "Alternative splicing of mouse IL-15 is due to the use of an internal
RT splice site in exon 5.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB022307; BAA37122.1; -.
DR EMBL; AJ012587; CAA10069.1; -.
DR MGD; MGI:103014; Il15.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1503 MW; 62A43C3889924E2B CRC64;

Query Match 26.3%; Score 5; DB 11; Length 14;

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  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSKEL 18
           |||||
Db       4 SSKEL 8


RESULT 2
Q16310
ID   Q16310      PRELIMINARY;      PRT;    17 AA.
AC   Q16310;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GC*2 protein (Fragment).
GN   GC*2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95242701; PubMed=7725672;
RA   Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT   "Characterization of mutants of the vitamin-D-binding protein/group
RT   specific component: GC aborigine (1A1) from Australian aborigines and
RT   South African blacks, and 2A9 from south Germany.";
RL   Vox Sang. 68:50-54(1995).
DR   EMBL; S77130; AAD14250.1; -.
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  1845 MW;  BB26CAD60293722C CRC64;

  Query Match            21.1%;  Score 4;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KELA 19
           ||||
Db       7 KELA 10


RESULT 3
Q13376
ID   Q13376      PRELIMINARY;      PRT;    17 AA.
AC   Q13376;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
     RNA binding motif (Fragment).
GN   RBM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97032533; PubMed=8875892;
RA   Prosser J., Inglis J.D., Condie A., Ma K., Kerr S., Thakrar R.,
RA   Taylor K., Cameron J.M., Cooke H.J.;
RT   "Degeneracy in human multicopy RBM (YRRM), a candidate spermatogenesis
RT   gene.";
RL   Mamm. Genome 7:835-842(1996).
DR   EMBL; U38450; AAB49815.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   17 AA;  2060 MW;  98CD6AEFEC350012 CRC64;

  Query Match            21.1%;  Score 4;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       3 GRGR 6


RESULT 4
Q16271
ID   Q16271      PRELIMINARY;      PRT;    19 AA.
AC   Q16271;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Arginine vasopressin V2 receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95086168; PubMed=7993996;
RA   Holtzman E.J., Kolakowski L.F.Jr., Geifman-Holtzman O., O'Brien D.G.,
RA   Rasoulpour M., Guillot A.P., Ausiello D.A.;
RT   "Mutations in the vasopressin V2 receptor gene in two families with
RT   nephrogenic diabetes insipidus.";
RL   J. Am. Soc. Nephrol. 5:169-176(1994).
DR   EMBL; S75754; AAB32753.1; -.
KW   Receptor.
FT   NON_TER      1      1
SQ   SEQUENCE   19 AA;  1905 MW;  181640EFD90F2788 CRC64;

  Query Match            21.1%;  Score 4;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPGH 5
           ||||
Db       1 VPGH 4


RESULT 5
Q9QUZ1
ID   Q9QUZ1      PRELIMINARY;      PRT;    20 AA.
AC   Q9QUZ1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Alpha class glutathione S-transferase subunit 2 (EC 2.5.1.18)
DE   (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96036981; PubMed=7485987;
RA   Rouimi P., Debrauwer L., Tulliez J.;
RT   "Electrospray ionization-mass spectrometry as a tool for
RT   characterization of glutathione S-transferase isozymes.";
RL   Anal. Biochem. 229:304-312(1995).
SQ   SEQUENCE   20 AA;  2412 MW;  9498D6E2C030B236 CRC64;

  Query Match            21.1%;  Score 4;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db      11 GRGR 14


RESULT 6
P83067
ID   P83067      PRELIMINARY;      PRT;    10 AA.
AC   P83067;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
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DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   82 kDa protein (Fragment).
OS   Bacillus cereus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Bacillaceae; Bacillus.
OX   NCBI_TaxID=1396;
RN   [1]
RP   SEQUENCE, AND INDUCTION.
RC   STRAIN=NCIMB 11796;
RA   Browne N., Dowds B.C.A.;
RL   Submitted (JUL-2001) to the SWISS-PROT data bank.
CC   -!- INDUCTION: BY SALT STRESS.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1200 MW;  72DBA14B1325AAEB CRC64;

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

      15 SKE 17
         |||
Db       5 SKE 7


RESULT 7
Q8RSU1
ID   Q8RSU1      PRELIMINARY;      PRT;    10 AA.
AC   Q8RSU1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Urease alpha subunit (EC 3.5.1.5) (Fragment).
GN   UREA.
OS   Helicobacter pylori (Campylobacter pylori).
OC   Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC   Helicobacter.
OX   NCBI_TaxID=210;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1061;
RA   van Vliet A.H.M., Poppelaars S.W., Davies B.J., Stoof J.,
RA   Bereswill S., Kist M., Penn C.W., Kuipers E.J., Kusters J.G.;
RT   "NikR mediates nickel-responsive transcriptional induction of urease
RT   expression in Helicobacter pylori.";
RL   Infect. Immun. 0:0-0(2002).
DR   EMBL; AY078177; AAL77213.1; -.
KW   Hydrolase.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1202 MW;  57C29E2B132771A7 CRC64;

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db       6 KEL 8


RESULT 8
P82937
ID   P82937      PRELIMINARY;      PRT;    10 AA.
AC   P82937;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Unknown endosperm protein B (Fragment).
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. BOMI; TISSUE=STARCHY ENDOSPERM;
RX   MEDLINE=21088911; PubMed=11271488;
RA   Kristoffersen H.E., Flengsrud R.;
RT   "Separation and characterization of basic barley seed proteins.";
RL   Electrophoresis 21:3693-3700(2000).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1297 MW;  8248A50B11FB5EBA CRC64;

  Query Match             15.8%;  Score 3;  DB 10;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 HER 7
            |||
Db       6 HER 8


RESULT 9
Q9QVF7
ID   Q9QVF7      PRELIMINARY;      PRT;    10 AA.
AC   Q9QVF7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Beta 2-glycoprotein I, beta 2-GPI (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92135065; PubMed=1777418;
RA   Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA   Yasuda T., Koike T.;
RT   "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT   cDNA cloning and inter-species differences of beta 2-GPI in
RT   alternation of anticardiolipin binding.";
RL   Int. Immunol. 3:1217-1221(1991).
FT   NON_TER       1       1
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1100 MW;  94E681B767376EA1 CRC64;

  Query Match             15.8%;  Score 3;  DB 11;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       1 GRT 3


RESULT 10
Q9QVE8
ID   Q9QVE8      PRELIMINARY;      PRT;    10 AA.
AC   Q9QVE8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Protamine MP2 intermediate protein PMP2/16 (Fragment).
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92174934; PubMed=1541289;
RA   Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT   "Molecular characterization of six intermediate proteins in the
RT   processing of mouse protamine P2 precursor.";
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```
RL   Eur. J. Biochem. 204:759-765(1992).
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1224 MW;  D4050B040B11EAB6 CRC64;

  Query Match             15.8%;  Score 3;  DB 11;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 HER 7
           |||
Db       5 HER 7


RESULT 11
Q9QVE7
ID   Q9QVE7      PRELIMINARY;      PRT;    10 AA.
AC   Q9QVE7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
     Protamine MP2 intermediate protein PMP2/20 (Fragment).
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92174934; PubMed=1541289;
RA   Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT   "Molecular characterization of six intermediate proteins in the
RT   processing of mouse protamine P2 precursor.";
RL   Eur. J. Biochem. 204:759-765(1992).
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1197 MW;  79920ED866DB1B04 CRC64;

  Query Match             15.8%;  Score 3;  DB 11;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 HER 7
           |||
Db       1 HER 3


RESULT 12
Q9UR95
ID   Q9UR95      PRELIMINARY;      PRT;    11 AA.
AC   Q9UR95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Heat shock protein 60 homolog (Fragment).
OS   Pichia angusta (Yeast) (Hansenula polymorpha).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Pichia.
OX   NCBI_TaxID=4905;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93223840; PubMed=8096822;
RA   Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA   Harder W., Veenhuis M.;
RT   "Affinity purification of molecular chaperones of the yeast Hansenula
RT   polymorpha using immobilized denatured alcohol oxidase.";
RL   FEBS Lett. 321:32-36(1993).
SQ   SEQUENCE   11 AA;  1230 MW;  71872C1779C3372B CRC64;

  Query Match             15.8%;  Score 3;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db       3 KEL 5


RESULT 13
O60614
ID   O60614      PRELIMINARY;      PRT;    11 AA.
AC   O60614;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MTG8 related protein (Fragment).
GN   MTGR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99009318; PubMed=9790752;
RA   Calabi F., Cilli V.;
RT   "CBFA2T1, a gene rearranged in human leukemia, is a member of a
RT   multigene family.";
RL   Genomics 52:332-341(1998).
DR   EMBL; AF052211; AAC64700.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1047 MW;  CF001CE4DDD86772 CRC64;

  Query Match             15.8%;  Score 3;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPG 4
           |||
Db       4 VPG 6


RESULT 14
Q9NY38
ID   Q9NY38      PRELIMINARY;      PRT;    11 AA.
AC   Q9NY38;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Heavy metal-responsive transcription factor (Fragment).
GN   MTF-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA   Georgiev O., Schaffner W.;
RT   "Characterization of the mouse gene for the heavy metal-responsive
RT   transcription factor MTF-1.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ251881; CAB71327.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1099 MW;  A8653693773772C6 CRC64;

  Query Match             15.8%;  Score 3;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRG 11
           |||
Db       8 GRG 10


RESULT 15
```

```
P83321
ID   P83321      PRELIMINARY;      PRT;    11 AA.
AC   P83321;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS   Penaeus monodon (Penoeid shrimp).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC   Penaeidae; Penaeus.
OX   NCBI_TaxID=6687;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=EYESTALK;
RA   Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA   Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT   "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT   of the giant tiger prawn Penaeus monodon.";
     Comp. Biochem. Physiol. 131B:325-337(2002).
     -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
     -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES      11      11       AMIDATION.
SQ   SEQUENCE   11 AA;  1301 MW;  9A19C860072DC771 CRC64;

  Query Match             15.8%;  Score 3;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       2 GRT 4


RESULT 16
Q9VN99
ID   Q9VN99      PRELIMINARY;      PRT;    11 AA.
AC   Q9VN99;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CG2676 protein.
GN   CG2676.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003603; AAF52049.1; -.
DR   FlyBase; FBgn0037309; CG2676.
SQ   SEQUENCE   11 AA;  1113 MW;  8760FE9BD5A1B1B1 CRC64;

  Query Match             15.8%;  Score 3;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       9 SSK 11


RESULT 17
P82698
ID   P82698      PRELIMINARY;      PRT;    11 AA.
AC   P82698;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Periviscerokinin-1 (LEM-PVK-1).
OS   Leucophaea maderae (Madeira cockroach),
OS   Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS   Blaberus craniifer,
OS   Blaptica dubia, and
OS   Gromphadorina portentosa (Cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC   TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX   MEDLINE=20307624; PubMed=10849006;
RA   Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT   "Identification of novel periviscerokinins from single neurohaemal
RT   release sites in insects. MS/MS fragmentation complemented by Edman
RT   degradation.";
RL   Eur. J. Biochem. 267:3869-3873(2000).
CC   -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC       (MYOTROPIC ACTIVITY).
CC   -!- MASS SPECTROMETRY: MW=1090.6; METHOD=MALDI.
KW   Neuropeptide; Amidation.
FT   MOD_RES      11      11       AMIDATION.
SQ   SEQUENCE   11 AA;  1091 MW;  2C2D80E2D7605728 CRC64;

  Query Match             15.8%;  Score 3;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       9 GRT 11
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```
RESULT 18
Q9TRW5
ID   Q9TRW5      PRELIMINARY;      PRT;    11 AA.
AC   Q9TRW5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   25 kDa protein P25, peptide F4 (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91372400; PubMed=1909972;
RA   Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA   Shiratsuchi A., Uchida T., Imahori K.;
     "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
     Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
     FEBS Lett. 289:37-43(1991).
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1276 MW;  CAF72DAF65A76AA9 CRC64;

  Query Match             15.8%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRG 11
           |||
Db       8 GRG 10


RESULT 19
Q04131
ID   Q04131      PRELIMINARY;      PRT;    11 AA.
AC   Q04131;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Wound induced protein (Fragment).
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
     NCBI_TaxID=4081;
     [1]
     SEQUENCE FROM N.A.
RC   STRAIN=PIK-RED; TISSUE=PERICARP;
RX   MEDLINE=91355936; PubMed=1715787;
RA   Parsons B.L., Mattoo A.K.;
RT   "Wound  regulated accumulation of specific transcripts in tomato
RT   fruit: interactions with fruit development, ethylene and light.";
RL   Plant Mol. Biol. 17:453-464(1991).
DR   EMBL; X59884; CAA42539.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   11 AA;  1278 MW;  92CB257828733325 CRC64;

  Query Match             15.8%;  Score 3;  DB 10;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       3 SSK 5


RESULT 20
Q99N81
ID   Q99N81      PRELIMINARY;      PRT;    11 AA.
AC   Q99N81;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Delta like 1 (Fragment).
GN   DLL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nakayama K.;
RT   "Multiple POU-binding motifs, recognized by tissue-specific nuclear
RT   factor(S), are important for Dll1 gene expression in developing neural
RT   precursor cells.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB050457; BAB43867.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1259 MW;  33C3634CBDC40B07 CRC64;

  Query Match             15.8%;  Score 3;  DB 11;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 MGR 10
           |||
Db       1 MGR 3


RESULT 21
Q9Z1H5
ID   Q9Z1H5      PRELIMINARY;      PRT;    11 AA.
AC   Q9Z1H5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Insulin receptor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94365199; PubMed=8083370;
RA   Huang Z., Bodkin N.L., Ortmeyer H.K., Hansen B.C., Shuldiner A.R.;
RT   "Hyperinsulinemia is associated with altered insulin receptor mRNA
RT   splicing in muscle of the spontaneously obese diabetic rhesus
RT   monkey.";
RL   J. Clin. Invest. 94:1289-1296(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ying L.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Liu Y.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L42997; AAC96365.1; -.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1052 MW;  9C25F7BAD8744865 CRC64;

  Query Match             15.8%;  Score 3;  DB 11;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSS 15
           |||
Db       2 TSS 4


RESULT 22
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```
Q89616
ID   Q89616      PRELIMINARY;      PRT;    11 AA.
AC   Q89616;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Hypothetical 1.2 kDa protein.
OS   Avian infectious bronchitis virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Coronaviridae; Coronavirus.
OX   NCBI_TaxID=11120;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87111468; PubMed=3027249;
RA   Boursnell M.E., Brown T.D.K., Foulds I.J., Green P.F., Tomley F.M.,
RA   Binns M.M.;
RT   "Completion of the sequence of the genome of the coronavirus avian
RT   infectious bronchitis virus.";
RL   J. Gen. Virol. 68:57-77(1987).
     [2]
     SEQUENCE FROM N.A.
     MEDLINE=88130171; PubMed=2829522;
RA   Boursnell M.E., Brown T.D., Foulds I.J., Green P.F., Tomley F.M.,
RA   Binns M.M.;
RT   "The complete nucleotide sequence of avian infectious bronchitis
RT   virus: analysis of the polymerase-coding region.";
RL   Adv. Exp. Med. Biol. 218:15-29(1987).
DR   EMBL; M94356; AAA46222.1; -.
DR   EMBL; M27471; AAA85340.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   11 AA;  1182 MW;  251EE3F165B721E8 CRC64;

  Query Match             15.8%;  Score 3;  DB 12;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 PGH 5
           |||
Db       3 PGH 5


RESULT 23
Q9DZ32
ID   Q9DZ32      PRELIMINARY;      PRT;    11 AA.
AC   Q9DZ32;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Gag polyprotein (Fragment).
GN   GAG.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20461476; PubMed=11005867;
RA   Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,
RA   Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
RA   Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA   Siliciano R., D'Aquila R.T.;
RT   "Antiretroviral resistance during successful therapy of HIV type 1
RT   infection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR   EMBL; AF292799; AAG25407.1; -.
KW   Polyprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   11 AA;  1386 MW;  79DC73C0145771B4 CRC64;

  Query Match             15.8%;  Score 3;  DB 15;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       3 GRT 5


RESULT 24
Q9K7A4
ID   Q9K7A4      PRELIMINARY;      PRT;    11 AA.
AC   Q9K7A4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein BH3464.
GN   BH3464.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
DR   EMBL; AP001518; BAB07183.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   11 AA;  1219 MW;  5F7D235CB7272B13 CRC64;

  Query Match             15.8%;  Score 3;  DB 16;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db       4 KEL 6


RESULT 25
O50303
ID   O50303      PRELIMINARY;      PRT;    12 AA.
AC   O50303;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 1.4 kDa protein (Fragment).
OS   Bacillus stearothermophilus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Geobacillus.
OX   NCBI_TaxID=1422;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CCM 2184;
RX   MEDLINE=20194845; PubMed=10732707;
RA   Vlaskova H., Krasny L., Fucik V., Jonak J.;
RT   "The pyrAb Gene Coding for the Large Subunit of Carbamoylphosphate
RT   Synthetase from Bacillus stearothermophilus: Molecular cloning and
RT   Functional Characterization.";
RL   Folia Biol. (Praha) 44:163-172(1998).
DR   EMBL; AJ001805; CAA05021.1; -.
KW   Hypothetical protein.
FT   NON_TER       12     12
SQ   SEQUENCE   12 AA;  1379 MW;  70087CB0E8A6840B CRC64;

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ERM 8
           |||
Db       5 ERM 7
```

Search completed: May 9, 2003, 16:07:38
Job time : 86 secs

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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:04:59 ; Search time 29 Seconds
(without alignments)
19.277 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

[redacted] size : 0

Total number of hits satisfying chosen parameters: 66571

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 10 | 52.6 | 10 | 2 | US-08-726-306A-1 | Sequence 1, Appli |
| 2 | 4 | 21.1 | 10 | 2 | US-08-482-228-202 | Sequence 202, App |
| 3 | 4 | 21.1 | 10 | 2 | US-08-310-912A-95 | Sequence 95, Appl |
| 4 | 4 | 21.1 | 10 | 3 | US-09-139-762A-39 | Sequence 39, Appl |
| 5 | 4 | 21.1 | 10 | 3 | US-09-139-762A-102 | Sequence 102, App |
| 6 | 4 | 21.1 | 10 | 3 | US-08-482-528-202 | Sequence 202, App |
| 7 | 4 | 21.1 | 10 | 3 | US-08-159-339A-669 | Sequence 669, App |
| 8 | 4 | 21.1 | 10 | 3 | US-08-841-089-95 | Sequence 95, Appl |
| 9 | 4 | 21.1 | 10 | 4 | US-09-301-085-95 | Sequence 95, Appl |
| 10 | 4 | 21.1 | 10 | 4 | US-09-479-431A-5 | Sequence 5, Appli |
| 11 | 4 | 21.1 | 10 | 5 | PCT-US95-04570-95 | Sequence 95, Appl |
| 12 | 4 | 21.1 | 10 | 5 | PCT-US95-04589-95 | Sequence 95, Appl |
| 13 | 4 | 21.1 | 10 | 6 | 5210075-7 | Patent No. 5210075 |
| 14 | 4 | 21.1 | 11 | 2 | US-08-960-128-5 | Sequence 5, Appli |
| 15 | 4 | 21.1 | 11 | 2 | US-08-350-260A-484 | Sequence 484, App |
| 16 | 4 | 21.1 | 11 | 3 | US-08-642-246-35 | Sequence 35, Appl |
| 17 | 4 | 21.1 | 11 | 4 | US-09-133-062D-26 | Sequence 26, Appl |
| 18 | 4 | 21.1 | 11 | 4 | US-09-297-981-18 | Sequence 18, Appl |
| 19 | 4 | 21.1 | 11 | 4 | US-09-451-206-35 | Sequence 35, Appl |
| 20 | 4 | 21.1 | 11 | 5 | PCT-US96-06229-35 | Sequence 35, Appl |
| 21 | 4 | 21.1 | 12 | 1 | US-08-548-540-155 | Sequence 155, App |
| 22 | 4 | 21.1 | 12 | 4 | US-08-687-590-5 | Sequence 5, Appli |
| 23 | 4 | 21.1 | 12 | 4 | US-09-461-697-439 | Sequence 439, App |
| 24 | 4 | 21.1 | 12 | 4 | US-09-297-981-30 | Sequence 30, Appl |
| 25 | 4 | 21.1 | 12 | 4 | US-07-946-180B-13 | Sequence 13, Appl |
| 26 | 4 | 21.1 | 12 | 5 | PCT-US96-09809-155 | Sequence 155, App |
| 27 | 4 | 21.1 | 13 | 1 | US-08-452-722-1 | Sequence 1, Appli |
| 28 | 4 | 21.1 | 13 | 1 | US-08-404-731A-1 | Sequence 1, Appli |
| 29 | 4 | 21.1 | 13 | 1 | US-08-344-227-1 | Sequence 1, Appli |
| 30 | 4 | 21.1 | 13 | 2 | US-08-503-226B-1 | Sequence 1, Appli |
| 31 | 4 | 21.1 | 13 | 3 | US-08-834-314-5 | Sequence 5, Appli |
| 32 | 4 | 21.1 | 13 | 3 | US-08-721-458B-1 | Sequence 1, Appli |
| 33 | 4 | 21.1 | 13 | 4 | US-08-444-818-129 | Sequence 129, App |
| 34 | 4 | 21.1 | 13 | 4 | US-09-155-941-14 | Sequence 14, Appl |
| 35 | 4 | 21.1 | 13 | 4 | US-09-155-941-18 | Sequence 18, Appl |
| 36 | 4 | 21.1 | 13 | 4 | US-09-155-941-22 | Sequence 22, Appl |
| 37 | 4 | 21.1 | 13 | 5 | PCT-US94-10257A-50 | Sequence 50, Appl |
| 38 | 4 | 21.1 | 14 | 1 | US-08-321-668-29 | Sequence 29, Appl |
| 39 | 4 | 21.1 | 14 | 1 | US-08-837-941-29 | Sequence 29, Appl |
| 40 | 4 | 21.1 | 14 | 2 | US-08-651-818A-20 | Sequence 20, Appl |
| 41 | 4 | 21.1 | 14 | 2 | US-08-722-806A-10 | Sequence 10, Appl |
| 42 | 4 | 21.1 | 14 | 4 | US-09-184-826-20 | Sequence 20, Appl |
| 43 | 4 | 21.1 | 14 | 4 | US-09-337-028-10 | Sequence 10, Appl |
| 44 | 4 | 21.1 | 14 | 4 | US-09-597-877-10 | Sequence 10, Appl |
| 45 | 4 | 21.1 | 14 | 5 | PCT-US93-06751-62 | Sequence 62, Appl |

ALIGNMENTS

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RESULT 1
US-08-726-306A-1
; Sequence 1, Application US/08726306A
; Patent No. 5958684
;  GENERAL INFORMATION:
;    APPLICANT:  van Leeuwen, Frederik Willem
;    APPLICANT:  Burbach, Johannes Peter Henri
;    APPLICANT:  Grosveld, Franklin G.
;    TITLE OF INVENTION:  DIAGNOSIS METHOD AND REAGENTS
;    NUMBER OF SEQUENCES:  189
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1 Financial Center
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,306A
;      FILING DATE:  02-Oct-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 95/20080.4
;      FILING DATE:  02-Oct-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/009,832
;      FILING DATE:  01-Jan-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  96,048-A (3255/00784)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-726-306A-1

  Query Match             52.6%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      10 RGRTSSKELA 19
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Db       1 RGRTSSKELA 10


RESULT 2
US-08-482-228-202
; Sequence 202, Application US/08482228
; Patent No. 5968753
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
:    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
     NUMBER OF SEQUENCES:  215
     CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
;      CITY:  Irvine
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92713-5210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,228
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Guthrie, Janice
;      REGISTRATION NUMBER:  35,170
;      REFERENCE/DOCKET NUMBER:  IT-4630CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 440-5353
;      TELEFAX:  (714) 553-1952
;  INFORMATION FOR SEQ ID NO:  202:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-228-202

  Query Match             21.1%;  Score 4;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSSK 16
           ||||
Db       6 TSSK 9


RESULT 3
US-08-310-912A-95
; Sequence 95, Application US/08310912A
; Patent No. 5981730
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  208
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2904
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,912A
;      FILING DATE:  September 22, 1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/227,360
;      FILING DATE:  April 13, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/254001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-310-912A-95

  Query Match             21.1%;  Score 4;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPGH 5
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Db       3 VPGH 6


RESULT 4
US-09-139-762A-39
; Sequence 39, Application US/09139762A
; Patent No. 6013453
;  GENERAL INFORMATION:
;    APPLICANT:  Choo, Yen
;    APPLICANT:  Klug, Aaron
;    APPLICANT:  Sanchez Garcia, Isidro
;    TITLE OF INVENTION:  Improvements in or Relating to
;    TITLE OF INVENTION:  Binding Proteins for Recognition of DNA
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/139,762A
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;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/793,408
;       FILING DATE:  02-JUN-1997
;       APPLICATION NUMBER:  PCT/GB95/01949
;       FILING DATE:  17-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9514698.1
;       FILING DATE:  18-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9422534.9
;       FILING DATE:  08-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9416880.4
;       FILING DATE:  20-AUG-1994
;   INFORMATION FOR SEQ ID NO:  39:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
        STRANDEDNESS:
        TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
US-09-139-762A-39

  Query Match             21.1%;  Score 4;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GHER 7
           ||||
Db       7 GHER 10


RESULT 5
US-09-139-762A-102
; Sequence 102, Application US/09139762A
; Patent No. 6013453
;  GENERAL INFORMATION:
;    APPLICANT:  Choo, Yen
;    APPLICANT:  Klug, Aaron
;    APPLICANT:  Sanchez Garcia, Isidro
;    TITLE OF INVENTION:  Improvements in or Relating to
;    TITLE OF INVENTION:  Binding Proteins for Recognition of DNA
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
       CITY:  Washington
       STATE:  D.C.
       COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/139,762A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/793,408
;      FILING DATE:  02-JUN-1997
;      APPLICATION NUMBER:  PCT/GB95/01949
;      FILING DATE:  17-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9514698.1
;      FILING DATE:  18-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9422534.9
;      FILING DATE:  08-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9416880.4
;      FILING DATE:  20-AUG-1994
;  INFORMATION FOR SEQ ID NO:  102:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-09-139-762A-102

  Query Match             21.1%;  Score 4;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GHER 7
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Db       7 GHER 10


RESULT 6
US-08-482-528-202
; Sequence 202, Application US/08482528
; Patent No. 6017719
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
;    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
;    NUMBER OF SEQUENCES:  215
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
;      CITY:  Irvine
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92713-5210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,528
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Guthrie, Janice
;      REGISTRATION NUMBER:  35,170
;      REFERENCE/DOCKET NUMBER:  IT-4630CIP4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 440-5353
;      TELEFAX:  (714) 553-1952
;  INFORMATION FOR SEQ ID NO:  202:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-528-202

  Query Match             21.1%;  Score 4;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSSK 16
           ||||
Db       6 TSSK 9
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RESULT 7
US-08-159-339A-669
; Sequence 669, Application US/08159339A
; Patent No. 6037135
;  GENERAL INFORMATION:
;    APPLICANT:  Kubo, Ralph T.
;    APPLICANT:  Grey, Howard M.
;    APPLICANT:  Sette, Alessandro
;    APPLICANT:  Celis, Esteban
;    TITLE OF INVENTION:  HLA Binding peptides and Their
;    TITLE OF INVENTION:  Uses
;    NUMBER OF SEQUENCES:  1254
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/159,339A
;      FILING DATE:  29-NOV-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/926,666
;      FILING DATE:  07-AUG-1992
;      APPLICATION NUMBER:  US 08/027,746
;      FILING DATE:  05-MAR-1993
;      APPLICATION NUMBER:  US 08/103,396
;      FILING DATE:  06-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  018623-005030US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  669:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-159-339A-669

  Query Match             21.1%;  Score 4;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 MGRG 11
           ||||
Db       5 MGRG 8


RESULT 8
US-08-841-089-95
; Sequence 95, Application US/08841089
; Patent No. 6127607
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE AND USES THEREOF
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2904
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/841,089
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,360
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/230001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-841-089-95

  Query Match             21.1%;  Score 4;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPGH 5
           ||||
Db       3 VPGH 6


RESULT 9
US-09-301-085-95
; Sequence 95, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
;  APPLICANT: Ausubel, Frederick M.
;  APPLICANT: Staskawicz, Brian J.
;  APPLICANT: Brent, Andrew F.
;  APPLICANT: Dahlbeck, Douglas
;  APPLICANT: Katagiri, Fumiaki
;  APPLICANT: Kunkel, Barbara N.
;  APPLICANT: Mindrinos, Michael N.
;  APPLICANT: Yu, Guo-Liang
;  TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
;  TITLE OF INVENTION: DETECTION  METHODS
;  FILE REFERENCE: 00786/254002
;  CURRENT APPLICATION NUMBER: US/09/301,085
;  CURRENT FILING DATE: 1999-04-28
;  EARLIER APPLICATION NUMBER: 08/310,912
;  EARLIER FILING DATE: 1994-09-22
;  EARLIER APPLICATION NUMBER: 08/227,360
;  EARLIER FILING DATE: 1994-04-13
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-95

Query Match 21.1%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VPGH 5
||||
Db 3 VPGH 6

RESULT 10
US-09-479-431A-5
; Sequence 5, Application US/09479431A
; Patent No. 6413556
; GENERAL INFORMATION:
; APPLICANT: Sky High, LLC
; APPLICANT: Bathurst, Ian C.
; APPLICANT: Foehr, Matthew
; TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
; FILE REFERENCE: 4147-23
; CURRENT APPLICATION NUMBER: US/09/479,431A
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: Xaa = any amino acid
US-09-479-431A-5

Query Match 21.1%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TSSK 16
||||
Db 2 TSSK 5

RESULT 11
PCT-US95-04570-95
; Sequence 95, Application PC/TUS9504570
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04570-95

Query Match 21.1%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VPGH 5
||||
Db 3 VPGH 6

RESULT 12
PCT-US95-04589-95
; Sequence 95, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04589
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070

```
;       TELEFAX:  (617) 542-8906
;       TELEX:  100254
;   INFORMATION FOR SEQ ID NO:  95:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-04589-95

  Query Match             21.1%;  Score 4;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPGH 5
            ||||
Db       3 VPGH 6


[redacted]ULT 13
5210075-7
;Patent No. 5210075
;     APPLICANT: SCHOLTZ, WOLFGANG;CHIANG, SHIU-LANG;NAGARAJAN,
;GOBI;LOBL, THOMAS J.
;     TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
;     NUMBER OF SEQUENCES: 69
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/480,868
;       FILING DATE: 16-FEB-1990
;SEQ ID NO:7:
;       LENGTH: 10
5210075-7

  Query Match             21.1%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSKE 17
            ||||
Db       2 SSKE 5


RESULT 14
US-08-960-128-5
; Sequence 5, Application US/08960128
; Patent No. 5951985
;  GENERAL INFORMATION:
[redacted];     APPLICANT:  Butler, Sandra M.
;     APPLICANT:  Pomato, Nicholas
;     APPLICANT:  Bos, Ebo
;     APPLICANT:  Hanna, Micheal G.
;     APPLICANT:  Haspel, Martin V.
;     APPLICANT:  Hoover, Herbert C.
;     TITLE OF INVENTION:  Tumor Associated Epitopes
;     NUMBER OF SEQUENCES:  7
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Akzo No. 5951985el Patent Department
;       STREET:  1300 Piccard Drive, Suite 206
;       CITY:  Rockville
;       STATE:  Maryland
;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/960,128
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,591
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Gormley, Mary E.
;       REGISTRATION NUMBER:  34,409
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (301) 258-5200
;       TELEFAX:  (301) 977-0847
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
US-08-960-128-5

  Query Match             21.1%;  Score 4;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
            ||||
Db       1 RTSS 4


RESULT 15
US-08-350-260A-484
; Sequence 484, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;     APPLICANT:  Winter, Gregory Paul
;     APPLICANT:  Griffiths, Andrew David
;     APPLICANT:  Williams, Samuel Cameron
;     APPLICANT:  Waterhouse, Peter
;     APPLICANT:  Nissim, Ahuva
;     APPLICANT:  Johnson, Kevin Stuart
;     APPLICANT:  Smith, Andrew John Hammond
;     TITLE OF INVENTION:  Methods for producing members of specific
;     TITLE OF INVENTION:  binding pairs
;     NUMBER OF SEQUENCES:  602
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David W. Clough
;       STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/350,260A
;       FILING DATE:  05-DEC-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9110549.4
;       FILING DATE:  15-MAY-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206318.9
;       FILING DATE:  24-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB91/01134
;       FILING DATE:  10-JUL-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB92/00883
;       FILING DATE:  15-MAY-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB93/00605
```

```
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  484:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-350-260A-484

  Query Match             21.1%;  Score 4;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       1 GRGR 4


RESULT 16
US-08-642-246-35
; Sequence 35, Application US/08642246
; Patent No. 6033654
;  GENERAL INFORMATION:
;    APPLICANT:  STEDRONSKY, Erwin R.
;    APPLICANT:  CAPPELLO, Joseph
;    TITLE OF INVENTION:  Tissue Adhesive Using Synthetic
;    TITLE OF INVENTION:  Crosslinking
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  Four Embarcadero Center, Suite 200
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
:    COMPUTER READABLE FORM:
       MEDIUM TYPE:  Floppy disk
       COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/642,246
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROWLAND, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  A61127-1/BIR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-642-246-35

  Query Match             21.1%;  Score 4;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       2 GRGR 5


RESULT 17
US-09-133-062D-26
; Sequence 26, Application US/09133062D
; Patent No. 6258776
; GENERAL INFORMATION:
;  APPLICANT:  Hemmings, Brian A
;  APPLICANT:  Millward, Thomas A
;  TITLE OF INVENTION:  Calcium Regulated Kinase
;  FILE REFERENCE:  30110
;  CURRENT APPLICATION NUMBER: US/09/133,062D
;  CURRENT FILING DATE:  1998-08-12
;  PRIOR APPLICATION NUMBER:  GB 9717089.8
;  PRIOR FILING DATE:  1997-08-12
;  PRIOR APPLICATION NUMBER:  GB 9717499.9
;  PRIOR FILING DATE:  1998-08-19
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
;   OTHER INFORMATION: internal peptide
US-09-133-062D-26

  Query Match             21.1%;  Score 4;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       4 RTSS 7


RESULT 18
US-09-297-981-18
; Sequence 18, Application US/09297981
; Patent No. 6362007
; GENERAL INFORMATION:
;  APPLICANT: MEHENS, LYDIE
;  APPLICANT: LUHRMANN, REINHARD GEORGE
;  APPLICANT: UNION, ANN
;  APPLICANT: RAYMACKERS, JOSEPH
;  TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE
;  TITLE OF INVENTION: ANTIBODIES FROM SERA OF LIVING BEINGS AFFECTED WITH
;  TITLE OF INVENTION: SYSTEMIC LUPUS ERYTHEMATOSUS
;  FILE REFERENCE: INNS011---
;  CURRENT APPLICATION NUMBER: US/09/297,981
;  CURRENT FILING DATE: 1999-05-10
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-297-981-18

  Query Match             21.1%;  Score 4;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
```

```
          ||||
Db      3 GRGR 6


RESULT 19
US-09-451-206-35
; Sequence 35, Application US/09451206
; Patent No. 6423333
;  GENERAL INFORMATION:
;       APPLICANT: STEDRONSKY, Erwin R.
;                  CAPPELLO, Joseph
;       TITLE OF INVENTION: Tissue Adhesive Using Synthetic
;                           Crosslinking
;       NUMBER OF SEQUENCES: 35
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;            STREET: Four Embarcadero Center, Suite 200
;            CITY: San Francisco
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/451,206
;            FILING DATE: 29-No. 6423333-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/642,246
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: ROWLAND, Bertram I
;            REGISTRATION NUMBER: 20015
;            REFERENCE/DOCKET NUMBER: A61127-1/BIR
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-781-1989
;            TELEFAX: 415-398-3249
;  INFORMATION FOR SEQ ID NO: 35:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 11 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 35:
;  US-09-451-206-35

  Query Match             21.1%;  Score 4;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 GRGR 12
          ||||
Db      2 GRGR 5


RESULT 20
PCT-US96-06229-35
; Sequence 35, Application PC/TUS9606229
;  GENERAL INFORMATION:
;    APPLICANT:  STEDRONSKY, Erwin R.
;    APPLICANT:  CAPPELLO, Joseph
;    TITLE OF INVENTION:  Tissue Adhesive Using Synthetic
;    TITLE OF INVENTION:  Crosslinking
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  Four Embarcadero Center, Suite 200
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/06229
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROWLAND, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  A61127-1/BIR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US96-06229-35

  Query Match             21.1%;  Score 4;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 GRGR 12
          ||||
Db      2 GRGR 5


RESULT 21
US-08-548-540-155
; Sequence 155, Application US/08548540
; Patent No. 5733731
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    APPLICANT:  Stemmer, Willem P.C.
;    APPLICANT:  Gates, Christian M.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  162
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/548,540
;      FILING DATE:  26-OCT-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/290,641
;      FILING DATE:  15-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,321
;      FILING DATE:  15-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
```

```
;      REFERENCE/DOCKET NUMBER:  16528J-001240US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  155:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-548-540-155

  Query Match            21.1%;  Score 4;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 RMGR 10
           ||||
Db       4 RMGR 7


RESULT 22
US-08-687-590-5
; Sequence 5, Application US/08687590
; Patent No. 6255070
;  GENERAL INFORMATION:
;    APPLICANT:  Willison, Keith Robert
;    APPLICANT:  Kubota, Hiroshi
;    APPLICANT:  Ashworth, Alan
;    TITLE OF INVENTION:  Folding Proteins
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,590
;      FILING DATE:  31-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/00192
;      FILING DATE:  31-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9401791.0
;      FILING DATE:  31-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9418234.2
;      FILING DATE:  09-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bastian, Kevin L.
;      REGISTRATION NUMBER:  34,774
;      REFERENCE/DOCKET NUMBER:  084619-000000US
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-687-590-5

  Query Match            21.1%;  Score 4;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       3 GRGR 6


RESULT 23
US-09-461-697-439
; Sequence 439, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 439
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-461-697-439

  Query Match            21.1%;  Score 4;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSKE 17
           ||||
Db       9 SSKE 12


RESULT 24
US-09-297-981-30
; Sequence 30, Application US/09297981
; Patent No. 6362007
; GENERAL INFORMATION:
;  APPLICANT: MEHENS, LYDIE
;  APPLICANT: LUHRMANN, REINHARD GEORGE
;  APPLICANT: UNION, ANN
;  APPLICANT: RAYMACKERS, JOSEPH
;  TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE
;  TITLE OF INVENTION: ANTIBODIES FROM SERA OF LIVING BEINGS AFFECTED WITH
;  TITLE OF INVENTION: SYSTEMIC LUPUS ERYTHEMATOSUS
;  FILE REFERENCE: INNS011---
;  CURRENT APPLICATION NUMBER: US/09/297,981
;  CURRENT FILING DATE: 1999-05-10
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-297-981-30

  Query Match            21.1%;  Score 4;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       5 GRGR 8
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RESULT 25
US-07-946-180B-13
; Sequence 13, Application US/07946180B
; Patent No. 6369203
; GENERAL INFORMATION:
; APPLICANT: Zeppezauer, Michael
; APPLICANT: Sch nberger, Arno
; APPLICANT: Cebecauer, Ladislav
; TITLE OF INVENTION: Peptides For The Production Of
; TITLE OF INVENTION: Preparations For The Diagnosis
; TITLE OF INVENTION: and Therapy Of Systemic Lupus
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rosenman & Colin
; STREET: 575 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10022-2585
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5"
; COMPUTER: IBM PS2-286
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,180B
; FILING DATE: 19920916
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 41 30 786.0
; FILING DATE: 09/16/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Weintraub, Bruce S.
; REGISTRATION NUMBER: 34,277
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 940-8800
; TELEFAX: (212) 940-8776/935-0679
; TELEX: 427571 ROSCOL (ITT)
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FRAGMENT TYPE: C-terminal fragment
; ORIGINAL SOURCE:
; ORGANISM: CALF
; TISSUE TYPE: THYMUS
; IMMEDIATE SOURCE: SYNTHETIC
; FEATURE:
; NAME/KEY: Peptide fragment
; NAME/KEY: 114-125 derived
; NAME/KEY: from histone H2B
; LOCATION: Location 1 through 12 below
; LOCATION: represents locations 114-125
; LOCATION: in the published sequence.
; IDENTIFICATION METHOD: By experiment
; PUBLICATION INFORMATION:
; AUTHORS: IWAI, K; et al;
; TITLE:
; JOURNAL: J.Biochem.
; VOLUME: 72
; PAGES: 357-367
; DATE: 1972
US-07-946-180B-13

Query Match 21.1%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TSSK 16
|||| |
Db 9 TSSK 12

Search completed: May 9, 2003, 16:08:14
Job time : 31 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:06:15 ; Search time 50 Seconds
(without alignments)
34.970 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 349150 seqs, 92025710 residues

1 size : 0

Total number of hits satisfying chosen parameters: 33076

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5 | 26.3 | 18 | 9 | US-10-270-877-33 | Sequence 33, Appl |
| 2 | 5 | 26.3 | 18 | 9 | US-10-270-837-33 | Sequence 33, Appl |
| 3 | 5 | 26.3 | 19 | 9 | US-10-117-846-33 | Sequence 33, Appl |
| 4 | 4 | 21.1 | 10 | 9 | US-10-040-572-5 | Sequence 5, Appli |
| 5 | 4 | 21.1 | 10 | 9 | US-09-185-908-119 | Sequence 119, App |
| 6 | 4 | 21.1 | 10 | 9 | US-09-185-908-128 | Sequence 128, App |
| 7 | 4 | 21.1 | 10 | 9 | US-09-185-908-137 | Sequence 137, App |
| 8 | 4 | 21.1 | 10 | 9 | US-09-185-908-146 | Sequence 146, App |
| 9 | 4 | 21.1 | 10 | 9 | US-09-185-908-155 | Sequence 155, App |
| 10 | 4 | 21.1 | 10 | 9 | US-09-899-046-219 | Sequence 219, App |
| 11 | 4 | 21.1 | 10 | 9 | US-09-899-046-220 | Sequence 220, App |
| 12 | 4 | 21.1 | 10 | 9 | US-09-899-046-221 | Sequence 221, App |
| 13 | 4 | 21.1 | 10 | 9 | US-09-878-281-219 | Sequence 219, App |
| 14 | 4 | 21.1 | 10 | 9 | US-09-878-281-220 | Sequence 220, App |
| 15 | 4 | 21.1 | 10 | 9 | US-09-878-281-221 | Sequence 221, App |
| 16 | 4 | 21.1 | 10 | 9 | US-09-572-404B-668 | Sequence 668, App |
| 17 | 4 | 21.1 | 10 | 9 | US-09-572-404B-670 | Sequence 670, App |
| 18 | 4 | 21.1 | 10 | 9 | US-09-572-404B-672 | Sequence 672, App |
| 19 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1028 | Sequence 1028, Ap |
| 20 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1300 | Sequence 1300, Ap |
| 21 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1302 | Sequence 1302, Ap |
| 22 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1368 | Sequence 1368, Ap |
| 23 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1484 | Sequence 1484, Ap |
| 24 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1576 | Sequence 1576, Ap |
| 25 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1580 | Sequence 1580, Ap |
| 26 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1582 | Sequence 1582, Ap |
| 27 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1720 | Sequence 1720, Ap |
| 28 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1722 | Sequence 1722, Ap |
| 29 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1732 | Sequence 1732, Ap |
| 30 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1784 | Sequence 1784, Ap |
| 31 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1843 | Sequence 1843, Ap |
| 32 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1845 | Sequence 1845, Ap |
| 33 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1847 | Sequence 1847, Ap |
| 34 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1849 | Sequence 1849, Ap |
| 35 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1851 | Sequence 1851, Ap |
| 36 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1853 | Sequence 1853, Ap |
| 37 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1855 | Sequence 1855, Ap |
| 38 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1857 | Sequence 1857, Ap |
| 39 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1859 | Sequence 1859, Ap |
| 40 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1861 | Sequence 1861, Ap |
| 41 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1863 | Sequence 1863, Ap |
| 42 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1865 | Sequence 1865, Ap |
| 43 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1867 | Sequence 1867, Ap |
| 44 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1869 | Sequence 1869, Ap |
| 45 | 4 | 21.1 | 10 | 9 | US-09-572-404B-1871 | Sequence 1871, Ap |

ALIGNMENTS

RESULT 1
US-10-270-877-33
; Sequence 33, Application US/10270877
; Publication No. US20030049791A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical
; OTHER INFORMATION: peptide
US-10-270-877-33

Query Match 26.3%; Score 5; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GRTSS 15
|||||
Db 14 GRTSS 18

RESULT 2
US-10-270-837-33
; Sequence 33, Application US/10270837
; Publication No. US20030054488A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2

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;  CURRENT APPLICATION NUMBER: US/10/270,837
;  CURRENT FILING DATE:  2002-10-11
;  PRIOR APPLICATION NUMBER: 09/512,563
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/121,483
;  PRIOR FILING DATE: 1999-02-24
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hypothetical
;   OTHER INFORMATION: peptide
US-10-270-837-33

  Query Match             26.3%;  Score 5;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTSS 15
           |||||
Db      14 GRTSS 18


RESULT 3
US-10-117-846-33
; Sequence 33, Application US/10117846
; Patent No. US20020168673A1
; GENERAL INFORMATION:
;  APPLICANT: Fuller, Margaret T
;  APPLICANT:  Hales, Karen G.
;  APPLICANT:  Santel, Ansgar H.
;  TITLE OF INVENTION: Mitofusins, Fzo Homologs and Functional
;  TITLE OF INVENTION:  Derivatives Thereof
;  FILE REFERENCE: STAN-063CIP3
;  CURRENT APPLICATION NUMBER: US/10/117,846
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/413,285
;  PRIOR FILING DATE: 1999-10-06
;  PRIOR APPLICATION NUMBER: PCT/US00/27871
;  PRIOR FILING DATE: 2000-10-06
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 19
    TYPE: PRT
    ORGANISM: Artificial Sequence
    FEATURE:
;   OTHER INFORMATION: consensus
US-10-117-846-33

  Query Match             26.3%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTSS 15
           |||||
Db       7 GRTSS 11


RESULT 4
US-10-040-572-5
; Sequence 5, Application US/10040572
; Patent No. US20020155183A1
; GENERAL INFORMATION:
;  APPLICANT: Sky High, LLC
;  APPLICANT:  Bathurst, Ian C.
;  APPLICANT:  Foehr, Matthew
;  TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
;  FILE REFERENCE: 4147-23-1
;  CURRENT APPLICATION NUMBER: US/10/040,572
;  CURRENT FILING DATE:  2002-03-12
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(10)
;   OTHER INFORMATION: Xaa = any amino acid
US-10-040-572-5

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSSK 16
           ||||
Db       2 TSSK 5


RESULT 5
US-09-185-908-119
; Sequence 119, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
;  APPLICANT: Blaschuk, Orest W.
;  APPLICANT: Gour, Barbara J.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
;  TITLE OF INVENTION: FUNCTIONS
;  FILE REFERENCE: 100086.409
;  CURRENT APPLICATION NUMBER: US/09/185,908A
;  CURRENT FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 269
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Product of
;   OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
;   FEATURE:
;   OTHER INFORMATION: Cyclic Peptide
US-09-185-908-119

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       3 RTSS 6


RESULT 6
US-09-185-908-128
; Sequence 128, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
;  APPLICANT: Blaschuk, Orest W.
;  APPLICANT: Gour, Barbara J.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
;  TITLE OF INVENTION: FUNCTIONS
;  FILE REFERENCE: 100086.409
;  CURRENT APPLICATION NUMBER: US/09/185,908A
;  CURRENT FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 269
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
;   LENGTH: 10
;   TYPE: PRT
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Product of
;   OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
;   FEATURE:
;   OTHER INFORMATION: Cyclic Peptide
US-09-185-908-128

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       3 RTSS 6


RESULT 7
US-09-185-908-137
; Sequence 137, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
;  APPLICANT: Blaschuk, Orest W.
;  APPLICANT: Gour, Barbara J.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
;  TITLE OF INVENTION: FUNCTIONS
;  FILE REFERENCE: 100086.409
;  CURRENT APPLICATION NUMBER: US/09/185,908A
;  CURRENT FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 269
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Product of
;   OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
;   FEATURE:
;   OTHER INFORMATION: Cyclic Peptide
US-09-185-908-137

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       3 RTSS 6


RESULT 8
US-09-185-908-146
; Sequence 146, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
;  APPLICANT: Blaschuk, Orest W.
;  APPLICANT: Gour, Barbara J.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
;  TITLE OF INVENTION: FUNCTIONS
;  FILE REFERENCE: 100086.409
;  CURRENT APPLICATION NUMBER: US/09/185,908A
;  CURRENT FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 269
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Product of
;   OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
;   FEATURE:
;   OTHER INFORMATION: Cyclic Peptide
US-09-185-908-146

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       3 RTSS 6


RESULT 9
US-09-185-908-155
; Sequence 155, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
;  APPLICANT: Blaschuk, Orest W.
;  APPLICANT: Gour, Barbara J.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
;  TITLE OF INVENTION: FUNCTIONS
;  FILE REFERENCE: 100086.409
;  CURRENT APPLICATION NUMBER: US/09/185,908A
;  CURRENT FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 269
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Product of
;   OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
;   FEATURE:
;   OTHER INFORMATION: Cyclic Peptide
US-09-185-908-155

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTSS 15
           ||||
Db       3 RTSS 6


RESULT 10
US-09-899-046-219
; Sequence 219, Application US/09899046
; Publication No. US20030008274A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
;    NUMBER OF SEQUENCES:  270
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/899,046
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  219:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
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US-09-899-046-219

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 11
US-09-899-046-220
; Sequence 220, Application US/09899046
; Publication No. US20030008274A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
     NUMBER OF SEQUENCES:  270
     COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/899,046
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  220:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-899-046-220

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7

ULT 12
US-09-899-046-221
; Sequence 221, Application US/09899046
; Publication No. US20030008274A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
;    NUMBER OF SEQUENCES:  270
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/899,046
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  221:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-899-046-221

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 13
US-09-878-281-219
; Sequence 219, Application US/09878281
; Publication No. US20030032005A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
;    NUMBER OF SEQUENCES:  270
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/878,281
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  219:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-878-281-219

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 14
US-09-878-281-220
; Sequence 220, Application US/09878281
; Publication No. US20030032005A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
;    NUMBER OF SEQUENCES:  270
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/878,281
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  220:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-878-281-220

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 15
US-09-878-281-221
; Sequence 221, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  New sequences of hepatitis C virus
;    TITLE OF INVENTION:  genotypes for diagnosis, prophylaxis and therapy.
;    NUMBER OF SEQUENCES:  270
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/878,281
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/362,455
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  221:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-878-281-221

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 16
US-09-572-404B-668
; Sequence 668, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 668
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in FXR1 at 428-437 and may interact with Sequend
;   OTHER INFORMATION: in this patent.
US-09-572-404B-668

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       4 GRGR 7


RESULT 17
US-09-572-404B-670
; Sequence 670, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 670
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in FXR1 at 427-436 and may interact with Sequ
;   OTHER INFORMATION: in this patent.
US-09-572-404B-670

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       5 GRGR 8


RESULT 18
US-09-572-404B-672
; Sequence 672, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 672
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in FXR1 at 428-437 and may interact with Sequ
;   OTHER INFORMATION: in this patent.
US-09-572-404B-672

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       4 GRGR 7


RESULT 19
```

```
US-09-572-404B-1028
; Sequence 1028, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1028
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in RPS29 at 42-51 and may interact with Sequence
;   OTHER INFORMATION: in this patent.
US-09-572-404B-1028

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       2 GRGR 5


RESULT 20
US-09-572-404B-1300
; Sequence 1300, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1300
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in FXR1 at 431-440 and may interact with Sequenc
;   OTHER INFORMATION: in this patent.
US-09-572-404B-1300

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       1 GRGR 4


RESULT 21
US-09-572-404B-1302
; Sequence 1302, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1302
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in FXR1 at 482-491 and may interact with Sequ
;   OTHER INFORMATION: in this patent.
US-09-572-404B-1302

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       6 GRGR 9


RESULT 22
US-09-572-404B-1368
; Sequence 1368, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1368
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in IL9 at 11-20 and may interact with Sequenc
;   OTHER INFORMATION: this patent.
US-09-572-404B-1368

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
Db       7 GRGR 10


RESULT 23
US-09-572-404B-1484
; Sequence 1484, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1484
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in RPS29 at 43-52 and may interact with Seque
;   OTHER INFORMATION: in this patent.
US-09-572-404B-1484

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRGR 12
           ||||
```

```
Db      1 GRGR 4


RESULT 24
US-09-572-404B-1576
; Sequence 1576, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1576
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: sequence located in KIAA0050 at 529-538 and may interact with Seq
;   OTHER INFORMATION: 1575 in this patent.
US-09-572-404B-1576

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 GRGR 12
          ||||
Db      4 GRGR 7


RESULT 25
US-09-572-404B-1580
; Sequence 1580, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
;  APPLICANT: Proteom Ltd
;  TITLE OF INVENTION: Complementary peptide ligands from the human genome
;  FILE REFERENCE: Human patent
;  CURRENT APPLICATION NUMBER: US/09/572,404B
;  CURRENT FILING DATE:  2000-05-17
;  NUMBER OF SEQ ID NOS: 4203
;  SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1580
;   LENGTH: 10
;   TYPE: PRT
    ORGANISM: Homo Sapiens
    FEATURE:
;   OTHER INFORMATION: sequence located in KIAA0064 at 333-342 and may interact with Seq
;   OTHER INFORMATION: 1579 in this patent.
US-09-572-404B-1580

  Query Match             21.1%;  Score 4;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 GRGR 12
          ||||
Db      6 GRGR 9


Search completed: May  9, 2003, 16:13:02
Job time : 51 secs
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 15:40:19 ; Search time 15 Seconds
(without alignments)
121.770 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

size : 0

Total number of hits satisfying chosen parameters: 3094

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 4 | 21.1 | 11 | 2 | PH0938 | T-cell receptor be |
| 2 | 4 | 21.1 | 12 | 2 | S68402 | NAD(+)-glycohydrol |
| 3 | 4 | 21.1 | 16 | 2 | PH0766 | T-cell receptor be |
| 4 | 4 | 21.1 | 18 | 2 | B24735 | glutathione transf |
| 5 | 4 | 21.1 | 20 | 2 | E60894 | crystallin - Pacif |
| 6 | 4 | 21.1 | 20 | 2 | S33001 | hypothetical prote |
| 7 | 4 | 21.1 | 20 | 2 | S48654 | Plasmepsin II - ma |
| 8 | 3 | 15.8 | 10 | 2 | PA0050 | protein QA100052 - |
| 9 | 3 | 15.8 | 10 | 2 | A27617 | triose-phosphate i |
| 10 | 3 | 15.8 | 10 | 2 | A42089 | transcription fact |
| 11 | 3 | 15.8 | 10 | 2 | B24736 | inhibin beta-B cha |
| 12 | 3 | 15.8 | 10 | 2 | PQ0785 | NADH2 dehydrogenas |
| 13 | 3 | 15.8 | 11 | 2 | PT0081 | protein QA300023 - |
| 14 | 3 | 15.8 | 11 | 2 | S19775 | wound-induced prot |
| 15 | 3 | 15.8 | 11 | 2 | PT0287 | Ig heavy chain CRD |
| 16 | 3 | 15.8 | 11 | 2 | I54193 | Rhesus blood group |
| 17 | 3 | 15.8 | 11 | 2 | S78422 | ribosomal protein |
| 18 | 3 | 15.8 | 11 | 2 | PH0939 | T-cell receptor be |
| 19 | 3 | 15.8 | 11 | 2 | H84082 | hypothetical prote |
| 20 | 3 | 15.8 | 12 | 2 | S26558 | T-cell receptor be |
| 21 | 3 | 15.8 | 12 | 2 | S65629 | protoporphyrinogen |
| 22 | 3 | 15.8 | 12 | 2 | A58501 | 24K kidney and bla |
| 23 | 3 | 15.8 | 12 | 2 | G49215 | urease (EC 3.5.1.5 |
| 24 | 3 | 15.8 | 12 | 2 | T44420 | hypothetical prote |
| 25 | 3 | 15.8 | 12 | 2 | A55837 | 5-aminoimidazole r |
| 26 | 3 | 15.8 | 12 | 2 | C30503 | Ig gamma-2b chain |
| 27 | 3 | 15.8 | 12 | 2 | PH1587 | Ig H chain V-D-J r |
| 28 | 3 | 15.8 | 12 | 2 | PH0931 | T-cell receptor be |
| 29 | 3 | 15.8 | 13 | 2 | A61288 | spore proteinase g |
| 30 | 3 | 15.8 | 13 | 2 | PT0331 | Ig heavy chain CRD |
| 31 | 3 | 15.8 | 13 | 2 | S54344 | glyceraldehyde-3-p |
| 32 | 3 | 15.8 | 14 | 1 | LFECW | trp operon leader |
| 33 | 3 | 15.8 | 14 | 1 | LFEBWC | trp operon leader |
| 34 | 3 | 15.8 | 14 | 1 | LFEBWT | trp operon leader |
| 35 | 3 | 15.8 | 14 | 2 | I51432 | histone H4-1 precu |
| 36 | 3 | 15.8 | 14 | 2 | A35377 | GTP-binding protei |
| 37 | 3 | 15.8 | 14 | 2 | E90858 | trp operon leader |
| 38 | 3 | 15.8 | 14 | 2 | PN0147 | omega-gliadine 1 a |
| 39 | 3 | 15.8 | 14 | 2 | PN0151 | omega-gliadine 2' |
| 40 | 3 | 15.8 | 14 | 2 | PC1215 | homeotic protein E |
| 41 | 3 | 15.8 | 14 | 2 | PL0152 | metal-binding prot |
| 42 | 3 | 15.8 | 14 | 2 | I64815 | carbonic anhydrase |
| 43 | 3 | 15.8 | 14 | 2 | PH1806 | T cell receptor al |
| 44 | 3 | 15.8 | 14 | 2 | B85761 | trp operon leader |
| 45 | 3 | 15.8 | 14 | 2 | F33160 | H+-transporting tw |

ALIGNMENTS

RESULT 1
PH0938
T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0938
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0938
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 21.1%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RGRT 13
||||
Db 6 RGRT 9

RESULT 2
S68402
NAD(+)-glycohydrolase - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 12-Dec-1997
C;Accession: S68402
R;Zhang, J.; Ziegler, M.; Schneider, R.; Klocker, H.; Auer, B.; Schweiger, M.
FEBS Lett. 377, 530-534, 1995
A;Title: Identification and purification of a bovine liver mitochondrial NAD(+)-glyco
A;Reference number: S68402; MUID:96140583; PMID:8549791
A;Accession: S68402
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7;8-12 <ZHA>
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; NAD

Query Match 21.1%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KELA 19
||||
Db 8 KELA 11

RESULT 3
PH0766
T-cell receptor beta chain (J3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0766
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0766
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60860; NID:g52745; PIDN:CAA43250.1; PID:g52746
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 21.1%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RGRT 13
||||
Db 6 RGRT 9

RESULT 4
B24735
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C;Accession: B24735
R;Mannervik, B.; Alin, P.; Guthenberg, C.; Jensson, H.; Tahir, M.K.; Warholm, M.; Jornva
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A;Title: Identification of three classes of cytosolic glutathione transferase common to
A;Reference number: A24735; MUID:86042634; PMID:3864155
A;Accession: B24735
A;Molecule type: protein
A;Residues: 1-18 <MAN>
C;Superfamily: glutathione transferase
C;Keywords: transferase

Query Match 21.1%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGR 12
||||
Db 11 GRGR 14

RESULT 5
E60894
crystallin - Pacific cuttlefish (fragment)
C;Species: Sepia esculenta (Pacific cuttlefish)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-1994
C;Accession: E60894
R;Chiou, S.H.
J. Protein Chem. 7, 527-534, 1988
A;Title: The protein sequence homology of gamma-crystallins among major vertebrate class
A;Reference number: A60894; MUID:89351593; PMID:3255376
A;Accession: E60894
A;Molecule type: protein
A;Residues: 1-20 <CHI>
C;Superfamily: glutathione transferase
C;Keywords: eye lens

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGR 12
||||
Db 10 GRGR 13

RESULT 6
S33001
hypothetical protein - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S33001
R;Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S33001
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <FAR>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24847.1; PID:g1334861

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 RTSS 15
||||
Db 9 RTSS 12

RESULT 7
S48654
Plasmepsin II - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jun-2000
C;Accession: S48654
R;Hill, J.; Tyas, L.; Phylip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.
FEBS Lett. 352, 155-158, 1994
A;Title: High level expression and characterisation of Plasmepsin II, an aspartic pro
A;Reference number: S48654; MUID:95010698; PMID:7925966
A;Accession: S48654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <HIL>

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MGRG 11
||||
Db 10 MGRG 13

RESULT 8
PA0050
protein QA100052 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0050; PA0107
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A;Reference number: PA0001
A;Accession: PA0050
A;Molecule type: protein
A;Residues: 1-10 <KAM>
R;Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A;Reference number: PA0109
A;Accession: PA0107
A;Molecule type: protein
A;Residues: 1-10 <KAW>
A;Experimental source: root

```
  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSS 15
           |||
Db       2 TSS 4


RESULT 9
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C;Accession: A27617
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A;Reference number: A94167
A;Accession: A27617
A;Molecule type: protein
A;Residues: 1-10 <BAU>
C;Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pentc

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       1 GRT 3


RESULT 10
A42089
transcription factor I-POU protein, alternative splice form - fruit fly (Drosophila mela
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C;Accession: A42089
R;Treacy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.G.
Cell 68, 491-505, 1992
A;Title: Twin of I-POU: a two amino acid difference in the I-POU homeodomain distinguish
A;Reference number: A42089; MUID:92154665; PMID:1346754
A;Accession: A42089
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <TRE>
A;Cross-references: GB:S82271; NID:g245517; PID:g245518
A;Note: sequence extracted from NCBI backbone (NCBIN:82267, NCBIN:82271, NCBIP:82273)
C;Genetics:
A;Gene: FlyBase:Ipou
A;Cross-references: FlyBase:FBgn0004418

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTS 14
           |||
Db       7 RTS 9


RESULT 11
B24736
inhibin beta-B chain - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993
C;Accession: B24736
R;Ling, N.; Ying, S.Y.; Ueno, N.; Esch, F.; Denoroy, L.; Guillemin, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 7217-7221, 1985
A;Reference number: A24736; MUID:86042637; PMID:3864157
A;Accession: B24736
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LIN>

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       6 GRT 8


RESULT 12
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)
N;Alternate names: complex I 27K chain; NADH-ubiquinone reductase 27K chain
C;Species: mitochondrion Vicia faba (fava bean)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
C;Accession: PQ0785
R;Leterme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A;Title: Purification and preliminary characterization of mitochondrial complex I (NA
A;Reference number: PQ0775; MUID:94151437; PMID:8108509
A;Accession: PQ0785
A;Molecule type: protein
A;Residues: 1-10 <LET>
C;Comment: Complex I, mitochondrial NADH-ubiquiquinone reductase, is the first of the
 ranging from 5K to 75K.
C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone
C;Genetics:
A;Genome: mitochondrion
C;Keywords: electron transfer; mitochondrion; oxidoreductase

  Query Match             15.8%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VPG 4
           |||
Db       3 VPG 5


RESULT 13
PT0081
protein QA300023 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C;Accession: PT0081
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization
A;Reference number: PN0173
A;Accession: PT0081
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: Leaf
C;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ser) #status experimental

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 SKE 17
           |||
Db       1 SKE 3


RESULT 14
S19775
wound-induced protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
```

```
C;Accession: S19775
R;Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       3 SSK 5


RESULT 15
PT0287
[redacted]eavy chain CRD3 region (clone 4-103) - human (fragment)
[redacted]pecies: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0287
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0287
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       5 GRT 7


RESULT 16
I54193
Rhesus blood group CcEe protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
[redacted]ccession: I54193
[redacted]erif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.
Genomics 19, 68-74, 1994
A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens
A;Reference number: I54193; MUID:94245182; PMID:8188244
A;Accession: I54193
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761
C;Genetics:
A;Gene: GDB:RHCE
A;Cross-references: GDB:229957; OMIM:111700
A;Map position: 1p36.2-1p34

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       2 SSK 4


RESULT 17
S78422
ribosomal protein RS20, mitochondrial [validated] - rat (tentative sequence) (fragmen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78422
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78422
A;Molecule type: protein
A;Residues: 1-11 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein S20
C;Keywords: mitochondrion; protein biosynthesis; ribosome

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      17 ELA 19
           |||
Db       4 ELA 6


RESULT 18
PH0939
T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0939
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0939
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       3 SSK 5


RESULT 19
H84082
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84082
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3464

  Query Match             15.8%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
```

```
Db      4 KEL 6


RESULT 20
S26558
T-cell receptor beta chain (clone Cw3/5B8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26558
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26558
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X68008
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSK 16
           |||
Db       3 SSK 5


RESULT 21
S65629
protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-May-2000
C;Accession: S65629
R;Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ind
Eur. J. Biochem. 230, 760-765, 1995
A;Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m
A;Reference number: S65629; MUID:95331315; PMID:7607249
A;Accession: S65629
A;Molecule type: protein
A;Residues: 1-12 <TAK>
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: heme biosynthesis; porphyrin biosynthesis
C;Superfamily: phytoene dehydrogenase
C;Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       1 GRT 3


RESULT 22
A58501
24K kidney and bladder stone protein 1 - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: A58501
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: A58501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <BIN>
A;Experimental source: human kidney and bladder stones
A;Note: tentative identification of 2-Ser

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 SKE 17
           |||
Db       2 SKE 4


RESULT 23
G49215
urease (EC 3.5.1.5) small subunit UreA - Helicobacter felis (fragment)
C;Species: Helicobacter felis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
C;Accession: G49215
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A;Title: Purification and characterization of the urease enzymes of Helicobacter spec
A;Reference number: A49215; MUID:93084378; PMID:1452359
A;Accession: G49215
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <TUR>
A;Experimental source: ATCC 49179
A;Note: sequence extracted from NCBI backbone (NCBIP:119489)
C;Keywords: hydrolase

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db       6 KEL 8


RESULT 24
T44420
hypothetical protein [imported] - Bacillus stearothermophilus (fragment)
C;Species: Bacillus stearothermophilus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T44420
R;Vlaskova, H.; Krasny, L.; Fucik, V.; Jonak, J.
submitted to the EMBL Data Library, September 1997
A;Description: The pyrAb gene coding for the large subunit of carbamoylphosphate synt
A;Reference number: Z22760
A;Accession: T44420
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-12 <VLA>
A;Cross-references: EMBL:AJ001805; PIDN:CAA05021.1
A;Experimental source: strain CCM 2184
C;Genetics:
A;Note: ORF2

  Query Match             15.8%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ERM 8
           |||
Db       5 ERM 7


RESULT 25
A55837
5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazo
C;Species: Gallus gallus (chicken)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C;Accession: A55837
```

R;Firestine, S.M.; Davisson, V.J.
Biochemistry 33, 11917-11926, 1994
A;Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal
A;Reference number: A55837; MUID:95001903; PMID:7918410
A;Accession: A55837
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FIR>

Query Match 15.8%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ELA 19
|||
Db 5 ELA 7

Search completed: May 9, 2003, 16:06:07
Job time : 18 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:39:44 ; Search time 10 Seconds
(without alignments)
78.805 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

d size : 0

Total number of hits satisfying chosen parameters: 916

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5 | 26.3 | 15 | 1 | UC08_MAIZE | P80614 zea mays (m |
| 2 | 3 | 15.8 | 10 | 1 | TPIS_NICPL | P19118 nicotiana p |
| 3 | 3 | 15.8 | 14 | 1 | ADF_TENMO | P82965 tenebrio mo |
| 4 | 3 | 15.8 | 14 | 1 | LPW_CITFR | P03056 citrobacter |
| 5 | 3 | 15.8 | 14 | 1 | LPW_ECOLI | P03053 escherichia |
| 6 | 3 | 15.8 | 14 | 1 | LPW_SALTY | P03054 salmonella |
| 7 | 3 | 15.8 | 14 | 1 | NEJ2_FASHE | P80526 fasciola he |
| 8 | 3 | 15.8 | 14 | 1 | PPK6_PERAM | P82693 periplaneta |
| 9 | 3 | 15.8 | 14 | 1 | TKN1_SCHGR | P82470 schistocerc |
| 10 | 3 | 15.8 | 15 | 1 | DCMM_PSECH | P19917 pseudomonas |
| 11 | 3 | 15.8 | 15 | 1 | ONC1_ONCMY | P83287 oncorhynchu |
| 12 | 3 | 15.8 | 16 | 1 | MMPX_SOLTU | P80501 solanum tub |
| 13 | 3 | 15.8 | 17 | 1 | VESP_VESMC | P57672 vespula mac |
| 14 | 3 | 15.8 | 18 | 1 | CPAX_BOVIN | P22779 bos taurus |
| 15 | 3 | 15.8 | 18 | 1 | GOME_ACAGO | P82358 acanthoscur |
| 16 | 3 | 15.8 | 19 | 1 | FIBB_HORSE | P14471 equus cabal |
| 17 | 3 | 15.8 | 19 | 1 | MIFH_TRIMR | P81530 trichuris m |
| 18 | 3 | 15.8 | 20 | 1 | ALAT_PIG | P13191 sus scrofa |
| 19 | 3 | 15.8 | 20 | 1 | EFTU_MYCSY | P81407 mycoplasma |
| 20 | 3 | 15.8 | 20 | 1 | ITRA_ALBJU | P24925 albizzia ju |
| 21 | 3 | 15.8 | 20 | 1 | LYC_FELCA | P37155 felis silve |
| 22 | 3 | 15.8 | 20 | 1 | MIF_PIG | P80928 sus scrofa |
| 23 | 3 | 15.8 | 20 | 1 | PORC_METTM | P80902 methanobact |
| 24 | 3 | 15.8 | 20 | 1 | PSBW_WHEAT | P55967 triticum ae |
| 25 | 3 | 15.8 | 20 | 1 | RIPX_CUCPE | P80750 cucurbita p |
| 26 | 3 | 15.8 | 20 | 1 | SAMP_PLEPL | P20677 pleuronecte |
| 27 | 2 | 10.5 | 10 | 1 | AMPN_HELAM | P81731 helicoverpa |
| 28 | 2 | 10.5 | 10 | 1 | BPP_VIPAS | P31351 vipera aspi |
| 29 | 2 | 10.5 | 10 | 1 | BRK_ONCMY | Q9prz1 oncorhynchu |
| 30 | 2 | 10.5 | 10 | 1 | COXH_ONCMY | P80331 oncorhynchu |
| 31 | 2 | 10.5 | 10 | 1 | COXK_ONCMY | P80332 oncorhynchu |
| 32 | 2 | 10.5 | 10 | 1 | COXO_RAT | P80432 rattus norv |
| 33 | 2 | 10.5 | 10 | 1 | COXO_THUOB | P80982 thunnus obe |
| 34 | 2 | 10.5 | 10 | 1 | COXQ_RABIT | P80336 oryctolagus |
| 35 | 2 | 10.5 | 10 | 1 | ESL_LACCA | P81758 lactobacill |
| 36 | 2 | 10.5 | 10 | 1 | FARP_MYTED | P42560 mytilus edu |
| 37 | 2 | 10.5 | 10 | 1 | GAJU_HUMAN | P01358 homo sapien |
| 38 | 2 | 10.5 | 10 | 1 | GLEM_HUMAN | P02728 homo sapien |
| 39 | 2 | 10.5 | 10 | 1 | GON1_ALLMI | P37041 alligator m |
| 40 | 2 | 10.5 | 10 | 1 | GON1_CHEPR | P80677 chelyosoma |
| 41 | 2 | 10.5 | 10 | 1 | GON1_CLUPA | P81749 clupea pall |
| 42 | 2 | 10.5 | 10 | 1 | GON1_PETMA | P04378 petromyzon |
| 43 | 2 | 10.5 | 10 | 1 | GON2_CHEPR | P80678 chelyosoma |
| 44 | 2 | 10.5 | 10 | 1 | GON2_CHICK | P37043 gallus gall |
| 45 | 2 | 10.5 | 10 | 1 | GON3_ONCKE | P20367 oncorhynchu |

ALIGNMENTS

RESULT 1
UC08_MAIZE
ID UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
DR Maize-2DPAGE; P80614; COLEOPTILE.
DR MaizeDB; 123934; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match 26.3%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VPGHE 6
|||||
Db 11 VPGHE 15

RESULT 2
TPIS_NICPL
ID TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE.

```
RA   Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT   "Alterations in the phenotype of plant cells studied by NH2-terminal
RT   amino acid-sequence analysis of proteins electroblotted from two-
RT   dimensional gel-separated total extracts.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC       phosphate.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC       AND PLASTID.
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   PIR; A27617; A27617.
DR   InterPro; IPR000652; Triophos_ismrse.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1140 MW;  80B9D37862C9C9D1 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db       1 GRT 3


RESULT 3
ADF_TENMO
ID   ADF_TENMO      STANDARD;      PRT;     14 AA.
AC   P82965;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Antidiuretic factor (ADF) (Antidiuretic hormone A) (ADHA).
OS   Tenebrio molitor (Yellow mealworm).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Cucujiformia; Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067;
RN   [1]
RP   SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC   TISSUE=Head;
RX   MEDLINE=21642653; PubMed=11756661;
RA   Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
     "Identification of a potent antidiuretic factor acting on beetle
     Malpighian tubules.";
     Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC   -!- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian
CC       tubules. Uses cGMP as a second messenger and inhibits fluid
CC       production by decreasing cAMP concentration.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC   -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC       PROTEIN LPCP29.
KW   Neuropeptide; Hormone.
SQ   SEQUENCE   14 AA;  1543 MW;  F49C91A3F16E43D1 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 PGH 5
            |||
Db       5 PGH 7


RESULT 4
LPW_CITFR
ID   LPW_CITFR      STANDARD;      PRT;     14 AA.
AC   P03056;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAY-1991 (Rel. 18, Last annotation update)
DE   Trp operon leader peptide.
GN   TRPL.
OS   Citrobacter freundii.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Citrobacter.
OX   NCBI_TaxID=546;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83007061; PubMed=6749821;
RA   Blumenberg M., Yanofsky C.;
RT   "Evolutionary divergence of the Citrobacter freundii tryptophan
RT   operon regulatory region: comparison with other enteric bacteria.";
RL   J. Bacteriol. 152:57-62(1982).
CC   -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC       OF TRYPTOPHAN.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; J01557; -; NOT_ANNOTATED_CDS.
DR   PIR; A03592; LFEBWC.
KW   Tryptophan biosynthesis; Leader peptide.
SQ   SEQUENCE   14 AA;  1720 MW;  5B792A473E8048E7 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTS 14
           |||
Db      12 RTS 14


RESULT 5
LPW_ECOLI
ID   LPW_ECOLI      STANDARD;      PRT;     14 AA.
AC   P03053;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Trp operon leader peptide.
GN   TRPL OR TRPEE OR B1265 OR Z2545 OR ECS1837.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82150258; PubMed=7038627;
RA   Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA   Horowitz H., van Cleemput M., Wu A.M.;
RT   "The complete nucleotide sequence of the tryptophan operon of
RT   Escherichia coli.";
RL   Nucleic Acids Res. 9:6647-6668(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=76240562; PubMed=781271;
RA   Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA   Yanofsky C.;
RT   "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT   Escherichia coli.";
RL   J. Mol. Biol. 103:351-381(1976).
RN   [3]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=80101455; PubMed=118451;
RA   Oxender D.L., Zurawski G., Yanofsky C.;
RT   "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT   secondary structure involving the tryptophan codon region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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CC   ---------------------------------------------------------------------
DR   EMBL; J01714; AAA57296.1; -.
DR   EMBL; A04494; CAA00361.1; -.
DR   EMBL; AE000224; AAC74347.1; -.
DR   EMBL; AE005380; AAG56550.1; -.
DR   EMBL; AP002556; BAB35260.1; -.
DR   PIR; A03589; LFECW.
DR   EcoGene; EG11274; trpL.
KW   Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ   SEQUENCE   14 AA;  1723 MW;  5B79306E3E804A37 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTS 14
           |||
Db      12 RTS 14


RESULT 6
LPW_SALTY
ID   LPW_SALTY      STANDARD;      PRT;    14 AA.
AC   P03054;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Trp operon leader peptide.
GN   TRPL OR TRPEE OR STM1722.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=78196931; PubMed=351195;
RA   Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT   "Comparison of the nucleotide sequences of the initial transcribed
RT   regions of the tryptophan operons of Escherichia coli and Salmonella
RT   typhimurium.";
RL   J. Mol. Biol. 121:193-217(1978).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M24960; -; NOT_ANNOTATED_CDS.
DR   EMBL; AE008776; AAL20640.1; -.
DR   PIR; A03590; LFEBWT.
DR   StyGene; SG10400; trpL.
KW   Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ   SEQUENCE   14 AA;  1635 MW;  49F22A47362248E7 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 RTS 14
           |||
Db      12 RTS 14


RESULT 7
NEJ2_FASHE
ID   NEJ2_FASHE     STANDARD;      PRT;    14 AA.
AC   P80526;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Newly excysted juvenile protein 2 (Fragment).
OS   Fasciola hepatica (Liver fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC   Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
OX   NCBI_TaxID=6192;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95366993; PubMed=7639732;
RA   Tkalcevic J., Ashman K., Meeusen E.;
RT   "Fasciola hepatica: rapid identification of newly excysted juvenile
```

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RT   proteins.";
RL   Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
CC       STAGE.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1581 MW;  9E0F0090CC8C0DF1 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     11 GRT 13
          |||
Db      5 GRT 7


RESULT 8
PPK6_PERAM
ID   PPK6_PERAM     STANDARD;      PRT;    14 AA.
AC   P82693;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pyrokinin-6 (Pea-PK-6) (FXPRL-amide).
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC   TISSUE=Abdominal perisympathetic organs, and Corpora cardiaca;
RX   MEDLINE=20189894; PubMed=10723010;
RA   Predel R., Eckert M.;
RT   "Tagma-specific distribution of FXPRLamides in the nervous system of
RT   the American cockroach.";
RL   J. Comp. Neurol. 419:352-363(2000).
CC   -!- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC   -!- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
CC       ABDOMINAL PERISYMPATHETIC ORGANS.
CC   -!- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.
CC   -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Amidation; Pyrokinin.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1592 MW;  3966CC3FF384A998 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 VPG 4
          |||
Db      5 VPG 7


RESULT 9
TKN1_SCHGR
ID   TKN1_SCHGR     STANDARD;      PRT;    14 AA.
AC   P82470;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tachykinin-1 (Scg-midgut-TK).
OS   Schistocerca gregaria (Desert locust).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC   Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC   Schistocerca.
OX   NCBI_TaxID=7010;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Midgut;
RX   MEDLINE=20050081; PubMed=10581195;
RA   Veelaert D., Baggerman G., Derua R., Waelkens E., Meeusen T.,
RA   Vande Water G., De Loof A., Schoofs L.;
RT   "Identification of a new tachykinin from the midgut of the desert
RT   locust, Schistocerca gregaria, by ESI-Qq-oa-TOF mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 266:237-242(1999).
CC   -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC       OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC   -!- TISSUE SPECIFICITY: MIDGUT.
CC   -!- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.
CC   -!- SIMILARITY: SIMILAR TO THE COCKROACH LEMTRP 3, A TACHYKININ-
CC       RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1496 MW;  CA4C578C0169FC72 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 VPG 4
          |||
Db      7 VPG 9


RESULT 10
DCMM_PSECH
ID   DCMM_PSECH     STANDARD;      PRT;    15 AA.
AC   P19917;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Carbon monoxide dehydrogenase medium chain (EC 1.2.99.2) (CO
DE   dehydrogenase subunit M) (CO-DH M) (Fragment).
GN   CUTM.
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Bradyrhizobium group.
OX   NCBI_TaxID=290;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC       dioxide.
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC       acceptor.
CC   -!- COFACTOR: FAD.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0143; PL0143.
KW   Oxidoreductase; Flavoprotein; FAD.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1815 MW;  90508CF93E739D63 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 PGH 5
          |||
Db      4 PGH 6


RESULT 11
ONC1_ONCMY
ID   ONC1_ONCMY     STANDARD;      PRT;    15 AA.
AC   P83287;
DT   15-JUN-2002 (Rel. 41, Created)
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DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Oncorhyncin 1 (Fragment).
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Skin;
RA   Fernandes J.M.O., Smith V.J., Kemp G.D.;
RT   "Purification and N-terminal sequencing of a 3 kDa antibacterial
RT   peptide from skin secretions of rainbow trout.";
RL   Submitted (MAY-2002) to the SWISS-PROT data bank.
CC   -!- FUNCTION: Has antibacterial activity against Gram-positive
CC       bacterium P.citreus.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
FT   Antibiotic.
FT   UNSURE        4      4       OR G.
FT   UNSURE        9      9       OR T.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1601 MW;  43C25028DBC12B7C CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      17 ELA 19
           |||
Db      11 ELA 13


RESULT 12
MMPX_SOLTU
ID   MMPX_SOLTU     STANDARD;      PRT;    16 AA.
AC   P80501;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Unidentified mitochondrial matrix protein (Fragment).
OS   Solanum tuberosum (Potato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4113;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Tuber;
RX   MEDLINE=97077345; PubMed=8919912;
RA   Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
RT   "New insights into the composition, molecular mass and stoichiometry
RT   of the protein complexes of plant mitochondria.";
RL   Plant J. 9:357-368(1996).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW   Mitochondrion.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1768 MW;  C58D4DB48AA18B8D CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 NVP 3
            |||
Db       3 NVP 5


RESULT 13
VESP_VESMC
ID   VESP_VESMC     STANDARD;      PRT;    17 AA.
AC   P57672;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Vespulakinin 1 [Contains: Vespulakinin 2].
OS   Vespula maculifrons (Eastern yellow jacket) (Wasp).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX   NCBI_TaxID=7453;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=76114777; PubMed=1247511;
RA   Yoshida H., Geller R.G., Pisano J.J.;
RT   "Vespulakinins: new carbohydrate-containing bradykinin derivatives.";
RL   Biochemistry 15:61-64(1976).
RN   [2]
RP   SYNTHESIS.
RX   MEDLINE=88057857; PubMed=3679673;
RA   Rocchi R., Biondi L., Filira F., Scolaro B.;
RT   "Synthesis, conformation, and biological activity of the carbohydrate-
RT   free vespulakinin 1.";
RL   Int. J. Pept. Protein Res. 30:240-256(1987).
CC   -!- FUNCTION: SMOOTH MUSCLE CONTRACTION.
CC   -!- SUBCELLULAR LOCATION: SECRETED; WASP VENOM RESERVOIRS.
CC   -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW   Bradykinin; Vasodilator; Venom; Glycoprotein.
FT   PEPTIDE       1     17       VESPULAKININ 1.
FT   PEPTIDE       3     17       VESPULAKININ 2.
FT   CARBOHYD      3      3       O-LINKED (GALNAC. . .).
FT   CARBOHYD      4      4       O-LINKED (GALNAC. . .).
SQ   SEQUENCE   17 AA;  1960 MW;  58B2CBA864122323 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 RGR 12
           |||
Db       7 RGR 9


RESULT 14
CPAX_BOVIN
ID   CPAX_BOVIN     STANDARD;      PRT;    18 AA.
AC   P22779;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91027757; PubMed=2121272;
RA   Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT   "Identification and biochemical analysis of novel olfactory-specific
RT   cytochrome P-450IIA and UDP-glucuronosyl transferase.";
RL   Biochemistry 29:7433-7440(1990).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC       NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC       OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC       ACIDS, AND XENOBIOTICS.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   PIR; A35704; A35704.
DR   InterPro; IPR001128; Cytochrome_P450.
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DR   PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum; Olfaction.
FT   NON_TER       1      1
FT   VARIANT       6      6       G -> D.
FT   VARIANT      11     11       A -> E.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2058 MW;  F80746F76CCD77FF CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db      13 KEL 15


RESULT 15
GOME_ACAGO
     GOME_ACAGO     STANDARD;      PRT;    18 AA.
     P82358;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Gomesin.
OS   Acanthoscurria gomesiana.
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Mygalomorphae; Theraphosidae; Acanthoscurria.
OX   NCBI_TaxID=115339;
RN   [1]
RP   SEQUENCE, MASS SPECTROMETRY, ACTIVITY, TISSUE SPECIFICITY, AMIDATION,
RP   AND DISULFIDE BONDS.
RC   TISSUE=Hemocyte;
RX   MEDLINE=20517902; PubMed=10942757;
RA   Silva P.I. Jr., Daffre S., Bulet P.;
RT   "Isolation and characterization of gomesin, an 18-residue cysteine-
RT   rich defense peptide from the spider Acanthoscurria gomesiana
RT   hemocytes with sequence similarities to horseshoe crab antimicrobial
RT   peptides of the tachyplesin family.";
RL   J. Biol. Chem. 275:33464-33470(2000).
CC   -!- FUNCTION: ACTIVE AGAINST SEVERAL GRAM-POSITIVE BACTERIA SUCH AS
CC       BACILLUS SPP, STAPHYLOCOCCUS SPP AND E.FAECALIS, SEVERAL GRAM-
CC       NEGATIVE BACTERIA SUCH AS E.COLI, K.PNEUMONIAE, P.AERUGINOSA AND
CC       SALMONELLA SPP, FILAMENTOUS FUNGI SUCH AS N.CRASSA, T.VIRIDAE
CC       AND YEASTS SUCH AS C.ALBICANS. IT IS ACTIVE AGAINST THE PARASITE
CC       L.AMAZONENSIS AS WELL. IT SHOWS HEMOLYTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: HEMOCYTES.
     -!- MASS SPECTROMETRY: MW=2270.4; METHOD=MALDI.
     Amidation; Antibiotic; Fungicide; Hemolysis.
     MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      18     18       AMIDATION.
FT   DISULFID      2     15
FT   DISULFID      6     11
SQ   SEQUENCE   18 AA;  2293 MW;  25ED499784908913 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 RGR 12
           |||
Db      16 RGR 18


RESULT 16
FIBB_HORSE
ID   FIBB_HORSE     STANDARD;      PRT;    19 AA.
AC   P14471;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN   FGB.
OS   Equus caballus (Horse), and
OS   Equus asinus (Donkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796, 9793;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Horse;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=E.asinus;
RA   Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT   "Structure of fibrinopeptides-its relation to enzyme specificity and
RT   phylogeny and classification of species.";
RL   Ark. Kemi 25:411-428(1966).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Plasma; Sulfation.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE B.
FT   MOD_RES       3      3       SULFATION.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2296 MW;  921A2B02D5F6891D CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRT 13
           |||
Db      10 GRT 12


RESULT 17
MIFH_TRIMR
ID   MIFH_TRIMR     STANDARD;      PRT;    19 AA.
AC   P81530;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory
DE   factor homolog) (Fragment).
OS   Trichuris muris.
OC   Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae;
OC   Trichuris.
OX   NCBI_TaxID=70415;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=99013685; PubMed=9794786;
RA   Pennock J.L., Behnke J.M., Bickle Q.D., Devaney E., Grencis R.K.,
RA   Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT   "Rapid purification and characterization of L-dopamine-methyl-ester
RT   tautomerase (macrophage migration inhibitory factor) from Trichinella
RT   spiralis, Trichuris muris and Brugia pahangi.";
RL   Biochem. J. 335:495-498(1998).
CC   -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC   -!- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR   InterPro; IPR001398; MIF.
DR   PROSITE; PS01158; MIF; PARTIAL.
KW   Cytokine.
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FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2058 MW;  F7D70C81D12F1234 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 NVP 3
           |||
Db       8 NVP 10


RESULT 18
ALAT_PIG
ID   ALAT_PIG       STANDARD;      PRT;    20 AA.
AC   P13191;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alanine aminotransferase (EC 2.6.1.2) (Glutamic--pyruvic transaminase)
DE   (GPT) (Glutamic--alanine transaminase) (Fragment).
GN   GPT OR GPT1 OR AAT1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=79232426; PubMed=465450;
RA   Tanase S., Kojima H., Morino Y.;
RT   "Pyridoxal 5'-phosphate binding site of pig heart alanine
RT   aminotransferase.";
RL   Biochemistry 18:3002-3007(1979).
CC   -!- FUNCTION: PARTICIPATES IN CELLULAR NITROGEN METABOLISM AND ALSO
CC       IN LIVER GLUCONEOGENESIS STARTING WITH PRECURSORS TRANSPORTED
CC       FROM SKELETAL MUSCLES.
CC   -!- CATALYTIC ACTIVITY: L-alanine + 2-oxoglutarate = pyruvate + L-
CC       glutamate.
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A
CC       MITOCHONDRIAL ONE.
CC   -!- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
DR   PIR; A14344; A14344.
KW   Transferase; Aminotransferase; Pyridoxal phosphate.
FT   NON_TER       1      1
FT   BINDING      11     11       PYRIDOXAL PHOSPHATE.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2217 MW;  1C2243A373EC4801 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      17 ELA 19
           |||
Db       2 ELA 4


RESULT 19
EFTU_MYCSY
ID   EFTU_MYCSY     STANDARD;      PRT;    20 AA.
AC   P81407;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Elongation factor Tu (EF-Tu) (Fragment).
GN   TUF.
OS   Mycoplasma synoviae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2109;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=ULB 925 / Isolate KF9;
RX   MEDLINE=99237234; PubMed=10220885;
RA   Bencina D., Narat M., Dovc P., Drobnic-Valic M., Habe F., Kleven S.H.;
RT   "The characterization of Mycoplasma synoviae EF-Tu protein and
RT   proteins involved in hemadherence and their N-terminal amino acid
RT   sequences.";
RL   FEMS Microbiol. Lett. 173:85-94(1999).
CC   -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC       AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC       BIOSYNTHESIS.
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC       EF-TU/EF-1A SUBFAMILY.
DR   InterPro; IPR000795; EF_GTPbind.
DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2222 MW;  C3C92564B740ACC6 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 SKE 17
           |||
Db       8 SKE 10


RESULT 20
ITRA_ALBJU
ID   ITRA_ALBJU     STANDARD;      PRT;    20 AA.
AC   P24925;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Trypsin inhibitor A chain (Fragment).
OS   Albizzia julibrissin (Silk tree).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizia.
OX   NCBI_TaxID=3813;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Seed;
RX   MEDLINE=80115605; PubMed=528539;
RA   Odani S., Ono T., Ikenaka T.;
RT   "Proteinase inhibitors from a mimosoideae legume, Albizzia
RT   julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL   J. Biochem. 86:1795-1805(1979).
CC   -!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
CC   -!- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC       DISULFIDE BOND.
CC   -!- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
CC       FAMILY.
DR   InterPro; IPR002160; Kunitz_legume.
DR   Pfam; PF00197; Kunitz_legume; 1.
DR   PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
KW   Serine protease inhibitor.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2191 MW;  1437376293377C25 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      16 KEL 18
           |||
Db       1 KEL 3
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RESULT 21
LYC_FELCA
ID   LYC_FELCA      STANDARD;      PRT;    20 AA.
AC   P37155;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Fragment).
GN   LYZ.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Milk;
RX   MEDLINE=90263403; PubMed=2344734;
RA   Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.;
RT   "Feline whey proteins: identification, isolation and initial
RT   characterization of alpha-lactalbumin, beta-lactoglobulin and
RT   lysozyme.";
RL   Comp. Biochem. Physiol. 95B:773-779(1990).
CC   -!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those
CC       in tissues and body fluids are associated with the monocyte-
CC       macrophage system and enhance the activity of immunoagents.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC       acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC       heteropolymers of the prokaryotes cell walls.
CC   -!- SUBUNIT: MONOMER.
CC   -!- MISCELLANEOUS: Lysozyme C is capable of both hydrolysis and
CC       transglycosylation; it shows also a slight esterase activity. It
CC       acts rapidly on both peptide-substituted and unsubstituted
CC       peptidoglycan, and slowly on chitin oligosaccharides.
CC   -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
DR   PIR; A60525; A60525.
DR   HSSP; P11376; 2EQL.
DR   InterPro; IPR001916; GH_22.
DR   Pfam; PF00062; lys; 1.
DR   PROSITE; PS00128; LACTALBUMIN_LYSOZYME; PARTIAL.
KW   Hydrolase; Glycosidase; Bacteriolytic enzyme; Milk.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2314 MW;  EB8824EA59425E13 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      17 ELA 19
           |||
Db       7 ELA 9


RESULT 22
MIF_PIG
ID   MIF_PIG        STANDARD;      PRT;    20 AA.
AC   P80928;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Glycosylation-inhibiting factor) (GIF) (Fragment).
GN   MIF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RA   Riviere S., Bouet F., Menez A., Galat A.;
RL   Submitted (MAR-1997) to the SWISS-PROT data bank.
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR   HSSP; P14174; 1GIF.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; PARTIAL.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine.
FT   ACT_SITE     1      1       CATALYTIC BASE (BY SIMILARITY).
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2147 MW;  3517AF60F3012A61 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 NVP 3
           |||
Db       8 NVP 10


RESULT 23
PORC_METTM
ID   PORC_METTM     STANDARD;      PRT;    20 AA.
AC   P80902;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Pyruvate synthase subunit PORC (EC 1.2.7.1) (Pyruvate oxidoreductase
DE   gamma chain) (POR) (Pyruvic-ferredoxin oxidoreductase gamma subunit)
DE   (Fragment).
GN   PORC.
OS   Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=79929;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=97261844; PubMed=9108258;
RA   Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT   "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT   in Methanobacterium thermoautotrophicum.";
RL   Eur. J. Biochem. 244:862-868(1997).
CC   -!- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE
CC       IS 80 DEGREES CELSIUS.
CC   -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC       CoA + CO(2) + reduced ferredoxin.
CC   -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC   -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC       GAMMA CHAIN.
CC   -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
KW   Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2167 MW;  481532134D42F353 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 GRG 11
           |||
Db       8 GRG 10


RESULT 24
PSBW_WHEAT
ID   PSBW_WHEAT     STANDARD;      PRT;    20 AA.
AC   P55967;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Photosystem II reaction center W protein (PSII 6.1 kDa protein)
DE   (Fragment).
```

```
GN   PSBW.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89121082; PubMed=2644131;
RA   Ikeuchi M., Takio K., Inoue Y.;
RT   "N-terminal sequencing of photosystem II low-molecular-mass proteins.
RT   5 and 4.1 kDa components of the O2-evolving core complex from higher
RT   plants.";
RL   FEBS Lett. 242:263-269(1989).
CC   -!- FUNCTION: SUBUNIT OF THE WATER OXIDATION COMPLEX OF PHOTOSYSTEM II
CC       REACTION CENTER COMPLEX.
CC   -!- SIMILARITY: BELONGS TO THE PSBW FAMILY.
KW   Photosynthesis; Photosystem II; Thylakoid; Membrane; Chloroplast.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2093 MW;  E26468763375B5C9 CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ERM 8
           |||
Db       4 ERM 6


RESULT 25
RIPX_CUCPE
ID   RIPX_CUCPE     STANDARD;      PRT;    20 AA.
AC   P80750;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ribosome-inactivating protein (rRNA N-glycosidase) (EC 3.2.2.22)
DE   (Fragment).
OS   Cucurbita pepo (Vegetable marrow) (Summer squash).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX   NCBI_TaxID=3663;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Mesocarp;
RX   MEDLINE=97175025; PubMed=9022685;
RA   Yoshinari S., Yokota S., Sawmoto H., Koresawa S., Tamura M.,
RA   Endo Y.;
RT   "Purification, characterization and subcellular localization of a
RT   type-1 ribosome-inactivating protein from the sarcocarp of Cucurbita
RT   pepo.";
RL   Eur. J. Biochem. 242:585-591(1996).
CC   -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC       specific adenosine on the 28S rRNA.
CC   -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC       TYPE 1 RIP SUBFAMILY.
DR   InterPro; IPR001574; RIP.
DR   Pfam; PF00161; RIP; 1.
DR   PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
KW   Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2235 MW;  8E753D217FDEAA6D CRC64;

  Query Match             15.8%;  Score 3;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 TSS 15
           |||
Db      10 TSS 12
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Search completed: May 9, 2003, 16:05:45
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:39:19 ; Search time 34 Seconds
(without alignments)
74.464 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGHERMGRGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

size : 0

Total number of hits satisfying chosen parameters: 158699

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 19 | 100.0 | 19 | 21 | AAY56391 | Mutant beta-APP pr |
| 2 | 15 | 78.9 | 19 | 22 | AAB99216 | AMY6 peptide. Uni |
| 3 | 13 | 68.4 | 14 | 22 | AAB99215 | AMY5 peptide. Uni |
| 4 | 12 | 63.2 | 12 | 21 | AAY56394 | Mutant beta-APP pr |
| 5 | 10 | 52.6 | 10 | 18 | AAW18633 | Peptide resulting |
| 6 | 10 | 52.6 | 10 | 19 | AAY20152 | Human beta-APP imm |
| 7 | 10 | 52.6 | 10 | 22 | AAB99214 | AMY1 peptide. Uni |
| 8 | 9 | 47.4 | 17 | 21 | AAY56393 | Mutant beta-APP pr |
| 9 | 8 | 42.1 | 15 | 21 | AAY56395 | Mutant ubiquitin-B |
| 10 | 5 | 26.3 | 10 | 21 | AAY85440 | Tumour antigen pro |
| 11 | 5 | 26.3 | 10 | 22 | AAG85559 | Saccharomyces cere |
| 12 | 5 | 26.3 | 10 | 22 | AAG85565 | Saccharomyces cere |
| 13 | 5 | 26.3 | 10 | 22 | AAG85579 | Saccharomyces cere |
| 14 | 5 | 26.3 | 14 | 22 | AAM98228 | Human peptide #150 |
| 15 | 5 | 26.3 | 15 | 22 | AAG66412 | G2 peptide. Unide |
| 16 | 5 | 26.3 | 18 | 21 | AAY95915 | Hypothetical signa |
| 17 | 5 | 26.3 | 19 | 22 | AAB47234 | hMnf1 Mitofusin GT |
| 18 | 4 | 21.1 | 10 | 14 | AAR37218 | IL-6 antagonist pe |
| 19 | 4 | 21.1 | 10 | 15 | AAR63388 | Hepatitis C virus |
| 20 | 4 | 21.1 | 10 | 15 | AAR63389 | Hepatitis C virus |
| 21 | 4 | 21.1 | 10 | 16 | AAW21262 | Hydroxymethylgluta |
| 22 | 4 | 21.1 | 10 | 17 | AAW12579 | SH2 binding peptid |
| 23 | 4 | 21.1 | 10 | 17 | AAW12570 | SH2 binding peptid |
| 24 | 4 | 21.1 | 10 | 20 | AAY55308 | CD34 antigen antig |
| 25 | 4 | 21.1 | 10 | 20 | AAY06153 | scFv 9A4 clone 23A |
| 26 | 4 | 21.1 | 10 | 20 | AAY14280 | Chemokine peptide, |
| 27 | 4 | 21.1 | 10 | 21 | AAB15835 | Human chemokine GR |
| 28 | 4 | 21.1 | 10 | 21 | AAB20860 | EMCV 3C protease u |
| 29 | 4 | 21.1 | 10 | 21 | AAB06530 | Claudin-2 cyclic c |
| 30 | 4 | 21.1 | 10 | 21 | AAB06539 | Claudin-2 cyclic c |
| 31 | 4 | 21.1 | 10 | 21 | AAB06548 | Claudin-2 cyclic c |
| 32 | 4 | 21.1 | 10 | 21 | AAB06557 | Claudin-2 cyclic c |
| 33 | 4 | 21.1 | 10 | 21 | AAB06566 | Claudin-2 cyclic c |
| 34 | 4 | 21.1 | 10 | 21 | AAY81338 | Streptavidin displ |
| 35 | 4 | 21.1 | 10 | 21 | AAY87054 | Human haematopoiet |
| 36 | 4 | 21.1 | 10 | 22 | ABP22811 | HIV A11 motif gag |
| 37 | 4 | 21.1 | 10 | 22 | AAM50167 | Monoclonal antibod |
| 38 | 4 | 21.1 | 10 | 22 | AAM43424 | Mycoplasma genital |
| 39 | 4 | 21.1 | 10 | 22 | AAG94474 | Human complementar |
| 40 | 4 | 21.1 | 10 | 22 | AAG94476 | Human complementar |
| 41 | 4 | 21.1 | 10 | 22 | AAG94478 | Human complementar |
| 42 | 4 | 21.1 | 10 | 22 | AAG94834 | Human complementar |
| 43 | 4 | 21.1 | 10 | 22 | AAG95106 | Human complementar |
| 44 | 4 | 21.1 | 10 | 22 | AAG95108 | Human complementar |
| 45 | 4 | 21.1 | 10 | 22 | AAG95174 | Human complementar |

ALIGNMENTS

RESULT 1
AAY56391
ID AAY56391 standard; peptide; 19 AA.
XX
AC AAY56391;
XX
DT 15-FEB-2000 (first entry)
XX
DE Mutant beta-APP protein peptide sequence SEQ ID NO:1.
XX
KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
KW gene therapy.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9958564-A1.
XX
PD 18-NOV-1999.
XX
PF 30-APR-1999; 99WO-NO00141.
XX
PR 08-MAY-1998; 98NO-0002098.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M;
XX
DR WPI; 2000-039070/03.
XX
PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
PT useful for treating Alzheimer's disease and Down syndrome -

XX
PS Claim 10; Page 27; 33pp; English.
XX
CC The present invention describes frameshift mutant beta-amyloid precursor
CC peptides (beta-APP) (AAY56391 to AAY56394) and mutant ubiquitin-B
CC (Ubi-B) (AAY56395 to AAY56400) associated with Alzheimer's disease and
CC Down syndrome eliciting T cellular immunity. The peptides may be used as
CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or
CC Ubi-B peptides that are associated with Alzheimer's disease or Down
CC syndrome. The patient may be stimulated in vivo or ex vivo with the
CC peptides. The peptides and DNA encoding the peptides can also be used for
CC the treatment or prophylaxis of Alzheimer's disease or the treatment of
CC Down syndrome.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NVPGHERMGRGRTSSKELA 19
||||||||||||||||||
Db 1 NVPGHERMGRGRTSSKELA 19

RESULT 2
AAB99216
ID AAB99216 standard; peptide; 19 AA.
XX
AC AAB99216;
XX
DT 06-SEP-2001 (first entry)
XX
DE AMY6 peptide.
XX
KW AMY6; disease detection; age-related disease; Alzheimer's disease;
KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Huntington's disease;
KW spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
KW beta-amyloid precursor protein; APP.
XX
OS Unidentified.
XX
PN WO200140804-A2.
XX
07-JUN-2001.

04-DEC-2000; 2000WO-NL00887.
XX
PR 03-DEC-1999; 99EP-0204140.
XX
PA (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
XX
PI Hol EM, Van Leeuwen FW;
XX
DR WPI; 2001-397965/42.
XX
PT Detecting a disease or pathological condition, associated with
PT secretion of aberrant protein e.g. age-related diseases, by determining
PT level of aberrant protein and/or its detectable part in body fluid
PT and/or tissue -
XX
PS Disclosure; Page 24; 36pp; English.
XX
CC The present invention relates to a method for detecting a disease or
CC pathological condition associated with molecular misreading of coding
CC sequences in the genome and/or associated with the clearance of aberrant
CC protein. The method comprises providing a sample of a body fluid and/or
CC tissue of a patient and determining a level of the aberrant protein
CC and/or its detectable part or the ratio between the two in the body fluid
CC and/or tissue. The method enables diagnosing the disease before the
CC patient exhibits clinical symptoms. The method is useful for diagnosing
CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or
CC other age related diseases e.g. cancer; neurodegenerative diseases, such
CC as frontal lobe dementia, progressive supranuclear palsy; and other
CC diseases with abundant tau-positive filamentous lesions, Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease,
CC spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
CC diseases associated with ubiquitin, diabetes mellitus type II and other
CC degenerative diseases such as cardiovascular diseases and rheumatoid
CC arthritis. A number of other diseases which can be diagnosed are given in
CC the specification. The present sequence is AMY 6 peptide, which was
CC coupled to thyroglobulin by glutardialdehyde, and used to immunise
CC rabbits for antibody production in the present invention. The AMY 6
CC peptide is a C-terminal fragment of the full-length beta-amyloid
CC precursor protein (APP+1; mature APP and its signal peptide) protein.
XX
SQ Sequence 19 AA;

Query Match 78.9%; Score 15; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HERMGRGRTSSKELA 19
|||||||||||||||
Db 5 HERMGRGRTSSKELA 19

RESULT 3
AAB99215
ID AAB99215 standard; peptide; 14 AA.
XX
AC AAB99215;
XX
DT 06-SEP-2001 (first entry)
XX
DE AMY5 peptide.
XX
KW AMY5; disease detection; age-related disease; Alzheimer's disease;
KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Huntington's disease;
KW spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
KW beta-amyloid precursor protein; APP.
XX
OS Unidentified.
XX
PN WO200140804-A2.
XX
PD 07-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-NL00887.
XX
PR 03-DEC-1999; 99EP-0204140.
XX
PA (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
XX
PI Hol EM, Van Leeuwen FW;
XX
DR WPI; 2001-397965/42.
XX
PT Detecting a disease or pathological condition, associated with
PT secretion of aberrant protein e.g. age-related diseases, by determining
PT level of aberrant protein and/or its detectable part in body fluid
PT and/or tissue -
XX
PS Disclosure; Page 24; 36pp; English.
XX
CC The present invention relates to a method for detecting a disease or
CC pathological condition associated with molecular misreading of coding
CC sequences in the genome and/or associated with the clearance of aberrant
CC protein. The method comprises providing a sample of a body fluid and/or
CC tissue of a patient and determining a level of the aberrant protein
CC and/or its detectable part or the ratio between the two in the body fluid

CC and/or tissue. The method enables diagnosing the disease before the
CC patient exhibits clinical symptoms. The method is useful for diagnosing
CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or
CC other age related diseases e.g. cancer; neurodegenerative diseases, such
CC as frontal lobe dementia, progressive supranuclear palsy; and other
CC diseases with abundant tau-positive filamentous lesions, Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease,
CC spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
CC diseases associated with ubiquitin, diabetes mellitus type II and other
CC degenerative diseases such as cardiovascular diseases and rheumatoid
CC arthritis. A number of other diseases which can be diagnosed are given in
CC the specification. The present sequence is AMY 5 peptide, which was
CC coupled to thyroglobulin by glutardialdehyde, and used to immunise
CC rabbits for antibody production in the present invention. The AMY 5
CC peptide is a C-terminal fragment of the full-length beta-amyloid
CC precursor protein (APP+1; mature APP and its signal peptide) protein.
XX
SQ Sequence 14 AA;

Query Match 68.4%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RMGRGRTSSKELA 19
||||||||||||| 
Db 2 RMGRGRTSSKELA 14

RESULT 4
AAY56394
ID AAY56394 standard; peptide; 12 AA.
XX
AC AAY56394;
XX
DT 15-FEB-2000 (first entry)
XX
DE Mutant beta-APP protein peptide sequence SEQ ID NO:4.
XX
KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
KW gene therapy.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9958564-A1.
XX
PD 18-NOV-1999.

30-APR-1999; 99WO-NO00141.

PR 08-MAY-1998; 98NO-0002098.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M;
XX
DR WPI; 2000-039070/03.
XX
PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
PT useful for treating Alzheimer's disease and Down syndrome -
XX
PS Claim 10; Page 27; 33pp; English.
XX
CC The present invention describes frameshift mutant beta-amyloid precursor
CC peptides (beta-APP) (AAY56391 to AAY56394) and mutant ubiquitin-B
CC (Ubi-B) (AAY56395 to AAY56400) associated with Alzheimer's disease and
CC Down syndrome eliciting T cellular immunity. The peptides may be used as
CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or
CC Ubi-B peptides that are associated with Alzheimer's disease or Down
CC syndrome. The patient may be stimulated in vivo or ex vivo with the
CC peptides. The peptides and DNA encoding the peptides can also be used for
CC the treatment or prophylaxis of Alzheimer's disease or the treatment of
CC Down syndrome.
XX
SQ Sequence 12 AA;

Query Match 63.2%; Score 12; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MGRGRTSSKELA 19
||||||||||||
Db 1 MGRGRTSSKELA 12

RESULT 5
AAW18633
ID AAW18633 standard; peptide; 10 AA.
XX
AC AAW18633;
XX
DT 21-JUL-1997 (first entry)
XX
DE Peptide resulting from human amyloid A4 gene +1 frameshift mutation.
XX
KW Frameshift mutation product; GAGA motif; somatic mutation; diagnosis;
KW detection; antibody; probe; cancer; neoplasia; neurodegenerative;
KW Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
KW Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;
KW PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
KW cardiovascular; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO9712992-A2.
XX
PD 10-APR-1997.
XX
PF 02-OCT-1996; 96WO-IB01106.
XX
PR 11-JAN-1996; 96US-0009832.
PR 02-OCT-1995; 95GB-0020080.
XX
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) UNIV STATE UTRECHT.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1997-226235/20.
XX
PT Use of mutant genes having frame:shift mutation(s) - for developing
PT prods. for the diagnosis, prevention and treatment of associated
PT diseases, e.g. cancer or neuro:degenerative disease
XX
PS Claim 24; Page 82; 123pp; English.
XX
CC AAW18633-W18641 are antigenic peptide products of +1 and +2 frameshift
CC mutations of various human genes including the amyloid A4, tau,
CC ubiquitin, apolipoprotein E, microtubule-associated protein 2
CC (MAP-2) and neurofilament subunit L, M and H genes. The peptides
CC are used for the production of antibodies which can be used in the
CC diagnosis, prevention and treatment of diseases such as cancer or
CC neurodegenerative disease, e.g. Parkinson's disease, Alzheimer's disease
CC Down's syndrome, frontal lobe dementia (Pick's disease), progressive
CC supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's
CC disease, multiple sclerosis, and other degenerative diseases such as
CC cardiovascular diseases and rheumatoid arthritis.
XX
SQ Sequence 10 AA;

Query Match 52.6%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      10 RGRTSSKELA 19
           ||||||||||
Db       1 RGRTSSKELA 10
```

RESULT 6
AAY20152
ID  AAY20152 standard; Peptide; 10 AA.
XX
AC  AAY20152;
XX
DT  22-JUL-1999  (first entry)
XX
DE  Human beta-APP immunogenic peptide fragment.
XX
KW  Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW  frameshift mutation; age-related disease; neurodegenerative disorder;
KW  Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW  Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW  diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW  ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW  neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW  glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW  bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW  high mobility group protein-C; neuroendocrine specific protein A;
KW  immunogenic.
XX
OS  Homo sapiens.
XX
PN  WO9845322-A2.
XX
PD  15-OCT-1998.
XX
PF  02-APR-1998;  98WO-IB00705.
XX
PR  10-APR-1997;  97US-0043163.
XX
PA  (UYUT-) RIJKSUNIV UTRECHT.
PA  (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA  (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI  Burbach JPH,  Grosveld FG,  Van Leeuwen FW;
XX
DR  WPI; 1998-609901/51.
XX
PT  Diagnosing disease by detecting frameshift mutations in RNA or
PT  corresponding protein mutations - used to diagnose cancer and
PT  neurological diseases, particularly Alzheimer's disease, and also
PT  for treatment and prevention with specific ribozymes or wild-type
PT  RNA
XX
PS  Claim 24; Page 85; 258pp; English.
XX
CC  This invention describes a novel method for the diagnosis of a disease
CC  caused by, or associated with, an RNA molecule that has a frameshift
CC  mutation. The method is used to diagnose age-related diseases, especially
CC  cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC  disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC  multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC  and many others listed) or susceptibility to these disorders. The method
CC  allows a definitive diagnosis of Alzheimer's disease in living patients,
CC  at an early stage. It is based on the observation that disease may be
CC  caused by mutations in RNA rather than DNA. The invention describes the
CC  used of neuronal system RNA molecules, specifically proteins including
CC  beta-amyloid precursor protein (beta-APP), the microtubule associated
CC  proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC  associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC  neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC  protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC  2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC  protein-C (HMGP-C) and neuroendocrine specific protein A.
XX

SQ  Sequence  10 AA;

```
  Query Match             52.6%;  Score 10;  DB 19;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00072;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 RGRTSSKELA 19
           ||||||||||
Db       1 RGRTSSKELA 10
```

RESULT 7
AAB99214
ID  AAB99214 standard; peptide; 10 AA.
XX
AC  AAB99214;
XX
DT  06-SEP-2001  (first entry)
XX
DE  AMY1 peptide.
XX
KW  AMY1; disease detection; age-related disease; Alzheimer's disease;
KW  Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KW  amyotrophic lateral sclerosis; Huntington's disease;
KW  spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
KW  degenerative disease; cardiovascular disease; rheumatoid arthritis;
KW  beta-amyloid precursor protein; APP.
XX
OS  Unidentified.
XX
PN  WO200140804-A2.
XX
PD  07-JUN-2001.
XX
PF  04-DEC-2000; 2000WO-NL00887.
XX
PR  03-DEC-1999;  99EP-0204140.
XX
PA  (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
XX
PI  Hol EM,  Van Leeuwen FW;
XX
DR  WPI; 2001-397965/42.
XX
PT  Detecting a disease or pathological condition, associated with
PT  secretion of aberrant protein e.g. age-related diseases, by determining
PT  level of aberrant protein and/or its detectable part in body fluid
PT  and/or tissue  -
XX
PS  Disclosure; Page 24; 36pp; English.
XX
CC  The present invention relates to a method for detecting a disease or
CC  pathological condition associated with molecular misreading of coding
CC  sequences in the genome and/or associated with the clearance of aberrant
CC  protein. The method comprises providing a sample of a body fluid and/or
CC  tissue of a patient and determining a level of the aberrant protein
CC  and/or its detectable part or the ratio between the two in the body fluid
CC  and/or tissue. The method enables diagnosing the disease before the
CC  patient exhibits clinical symptoms. The method is useful for diagnosing
CC  age-related diseases, preferably Alzheimer's disease, Down's syndrome or
CC  other age related diseases e.g. cancer; neurodegenerative diseases, such
CC  as frontal lobe dementia, progressive supranuclear palsy; and other
CC  diseases with abundant tau-positive filamentous lesions, Parkinson's
CC  disease, amyotrophic lateral sclerosis, Huntington's disease,
CC  spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
CC  diseases associated with ubiquitin, diabetes mellitus type II and other
CC  degenerative diseases such as cardiovascular diseases and rheumatoid
CC  arthritis. A number of other diseases which can be diagnosed are given in
CC  the specification. The present sequence is AMY 1 peptide, which was
CC  coupled to thyroglobulin by glutardialdehyde, and used to immunise
CC  rabbits for antibody production in the present invention. The AMY 1
CC  peptide is a C-terminal fragment of the full-length beta-amyloid
CC  precursor protein (APP+1; mature APP and its signal peptide) protein.

```
XX
SQ   Sequence   10 AA;

  Query Match             52.6%;  Score 10;  DB 22;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00072;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     10 RGRTSSKELA 19
          ||||||||||
Db      1 RGRTSSKELA 10


RESULT 8
AAY56393
ID   AAY56393 standard; peptide; 17 AA.
XX
AC   AAY56393;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Mutant beta-APP protein peptide sequence SEQ ID NO:3.
XX
KW   Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW   Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
KW   gene therapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9958564-A1.
XX
PD   18-NOV-1999.
XX
PF   30-APR-1999;   99WO-NO00141.
XX
PR   08-MAY-1998;   98NO-0002098.
XX
PA   (NHYD ) NORSK HYDRO AS.
XX
PI   Gaudernack G,  Eriksen JA,  Moller M;
XX
DR   WPI; 2000-039070/03.
XX
PT   Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
PT   useful for treating Alzheimer's disease and Down syndrome  -
XX
PS   Claim 10; Page 27; 33pp; English.
XX
CC   The present invention describes frameshift mutant beta-amyloid precursor
CC   peptides (beta-APP) (AAY56391 to AAY56394) and mutant ubiquitin-B
CC   (Ubi-B) (AAY56395 to AAY56400) associated with Alzheimer's disease and
CC   Down syndrome eliciting T cellular immunity. The peptides may be used as
CC   a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
CC   sufficient to induce specific T-cell immunity to mutant beta-APP and/or
CC   Ubi-B peptides that are associated with Alzheimer's disease or Down
CC   syndrome. The patient may be stimulated in vivo or ex vivo with the
CC   peptides. The peptides and DNA encoding the peptides can also be used for
CC   the treatment or prophylaxis of Alzheimer's disease or the treatment of
CC   Down syndrome.
XX
SQ   Sequence   17 AA;

  Query Match             47.4%;  Score 9;  DB 21;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 NVPGHERMG 9
          |||||||||
Db      9 NVPGHERMG 17


RESULT 9
AAY56395
ID   AAY56395 standard; peptide; 15 AA.
XX
AC   AAY56395;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Mutant ubiquitin-B peptide sequence SEQ ID NO:5.
XX
KW   Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW   Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
KW   gene therapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9958564-A1.
XX
PD   18-NOV-1999.
XX
PF   30-APR-1999;   99WO-NO00141.
XX
PR   08-MAY-1998;   98NO-0002098.
XX
PA   (NHYD ) NORSK HYDRO AS.
XX
PI   Gaudernack G,  Eriksen JA,  Moller M;
XX
DR   WPI; 2000-039070/03.
XX
PT   Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
PT   useful for treating Alzheimer's disease and Down syndrome  -
XX
PS   Claim 10; Page 27; 33pp; English.
XX
CC   The present invention describes frameshift mutant beta-amyloid precursor
CC   peptides (beta-APP) (AAY56391 to AAY56394) and mutant ubiquitin-B
CC   (Ubi-B) (AAY56395 to AAY56400) associated with Alzheimer's disease and
CC   Down syndrome eliciting T cellular immunity. The peptides may be used as
CC   a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
CC   sufficient to induce specific T-cell immunity to mutant beta-APP and/or
CC   Ubi-B peptides that are associated with Alzheimer's disease or Down
CC   syndrome. The patient may be stimulated in vivo or ex vivo with the
CC   peptides. The peptides and DNA encoding the peptides can also be used for
CC   the treatment or prophylaxis of Alzheimer's disease or the treatment of
CC   Down syndrome.
XX
SQ   Sequence   15 AA;

  Query Match             42.1%;  Score 8;  DB 21;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 RMGRGRTS 14
          ||||||||
Db      8 RMGRGRTS 15


RESULT 10
AAY85440
ID   AAY85440 standard; peptide; 10 AA.
XX
AC   AAY85440;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Tumour antigen protein SART-3 peptide derivative #20.
XX
KW   Tumour antigen protein; SART-3; cytotoxic T-cell; HLA antigen; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200012701-A1.
XX
```

PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-JP04622.
XX
PR 28-AUG-1998; 98JP-0242660.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Nakao M;
XX
DR WPI; 2000-237868/20.
XX
PT Tumor antigen protein SART-3 recognized by cytotoxic T-cells binding to
PT HLA antigen for treatment and diagnosis of tumors -
XX
PS Claim 11; Page 68; 89pp; Japanese.
XX
CC The invention provides a tumour antigen protein (SART-3) which is
CC recognized by cytotoxic T-cells binding to HLA antigen. SART-3 can be
CC expressed by standard recombinant methodology. SART-3 and its peptide
CC derivatives can be used in the prevention, treatment and diagnosis of
CC tumours in vitro or in vivo. Sequences AAY85423-484 represent peptide
CC derivatives of SART-3.
XX
SQ Sequence 10 AA;

Query Match 26.3%; Score 5; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SSKEL 18
|||||
Db 6 SSKEL 10

RESULT 11
AAG85559
ID AAG85559 standard; Peptide; 10 AA.
XX
AC AAG85559;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 508.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 3; Page 100; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;

Query Match 26.3%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGRT 13
|||||
Db 6 GRGRT 10

RESULT 12
AAG85565
ID AAG85565 standard; Peptide; 10 AA.
XX
AC AAG85565;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 514.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 3; Page 100; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;

Query Match 26.3%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGRT 13
|||||
Db 6 GRGRT 10

RESULT 13
AAG85579

ID AAG85579 standard; Peptide; 10 AA.
XX
AC AAG85579;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 528.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 3; Page 102; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;

Query Match 26.3%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGRT 13
||||| 
Db 6 GRGRT 10

RESULT 14
AAM98228
ID AAM98228 standard; Peptide; 14 AA.
XX
AC AAM98228;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1503 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 3997; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
SQ Sequence 14 AA;

Query Match 26.3%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RGRTS 14
||||| 
Db 3 RGRTS 7

RESULT 15
AAG66412
ID AAG66412 standard; Peptide; 15 AA.
XX
AC AAG66412;
XX
DT 22-OCT-2001 (first entry)
XX
DE G2 peptide.
XX
KW G protein 44; cancer; HIV infection; cytostatic; anti-HIV; G2.
XX
OS Unidentified.
XX
PN CN1296958-A.
XX
PD 30-MAY-2001.
XX
PF 22-NOV-1999; 99CN-0124046.
XX
PR 22-NOV-1999; 99CN-0124046.
XX
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX

PI Mao Y, Xie Y;
XX
DR WPI; 2001-489557/54.
XX
PT Polypeptide-human G protein 44 and polynucleotide for coding
PT polypeptide, useful for treating e.g. cancer and HIV infection, is
PT prepared by DNA recombination -
XX
PS Disclosure; Page 2 (Disclosure); 34pp; Chinese.
XX
CC The present invention relates to human G protein 44 and its coding
CC sequence (see AAH75817 and AAG66409). The G protein and its coding
CC sequence are useful for treating e.g. cancer and HIV infection. The
CC present peptide, G2 peptide, was used in the present invention.
XX
SQ Sequence 15 AA;

Query Match 26.3%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GRTSS 15
||||| 
Db 9 GRTSS 13

RESULT 16
AAY95915
ID AAY95915 standard; Peptide; 18 AA.
XX
AC AAY95915;
XX
DT 20-NOV-2000 (first entry)
XX
DE Hypothetical signal region of GPBP.
XX
KW Goodpasture antigen binding protein; GPBP; autoimmune disease;
KW apoptosis; cancer; tumour; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200050607-A2.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-IB00324.
XX
24-FEB-1999; 99US-0121483.

(SAUS/) SAUS J.
XX
PI Saus J;
XX
DR WPI; 2000-572094/53.
XX
PT Novel Goodpasture antigen binding proteins useful for diagnosing and
PT treating autoimmune disorders, tumor, and preventing cell apoptosis -
XX
PS Example 1; Page 31; 158pp; English.
XX
CC This peptide represents a portion of a hypothetical polypeptide
CC encoded by an open reading frame upstream of the human Goodpasture
CC antigen binding protein (GPBP) gene. An mRNA editing process
CC inserting a single bp (U) would generate an operative in-frame
CC start site and an open reading frame of 743 residues containing
CC an export signal immediately downstream of the editied Met.
CC Polyclonal antibodies raised against the peptide displayed a
CC linear vascular reactivity in human tissues suggestive of an
CC extracellular basement membrane localisation. GPBP (see AAY95900)
CC is a novel serine/threonine kinase that specifically binds to and
CC phosphorylates the N-terminus of Goodpasture antigen. The
CC invention provides nucleic acids (see AAA50341-53) encoding GPBP,
CC recombinant vectors, host cells, encoded polypeptides (see
CC AAY95900-11) and antibodies. It also provides methods for detecting
CC the presence of an autoimmune condition or apoptosis by detecting
CC an increase in GPBP expression, and methods for treating an
CC autoimmune disorder, apoptosis or a tumour by modifying GPBP
CC expression or activity.
XX
SQ Sequence 18 AA;

Query Match 26.3%; Score 5; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GRTSS 15
||||| 
Db 14 GRTSS 18

RESULT 17
AAB47234
ID AAB47234 standard; Peptide; 19 AA.
XX
AC AAB47234;
XX
DT 18-JUL-2001 (first entry)
XX
DE hMnf1 Mitofusin GTPase motif G1.
XX
KW Mitofusin; homolog; GTPase; mediation; mitochondrial fusion; stroke;
KW post-meiotic fusion; mitochondria; spermatid; anti-insect; deafness;
KW antifungal; fertility; mortality; arthropod pest; Leigh's syndrome;
KW mitochondrial disease; muscle myopathy; neurodegenerative disorder;
KW aging; Alzheimer's disease; Parkinsonian's disease; cancer; psoriasis;
KW autoimmune disease; diabetes mellitus; congenital muscular dystrophy;
KW fatal infantile myopathy; mitochondrial encephalopathy; optic atrophy;
KW lactic acidosis; mitochondrial diabetes; neuropathy; osteoarthritis;
KW progressive external ophthalmoplegia; dystonia; schizophrenia.
XX
OS Homo sapiens.
XX
PN WO200125274-A1.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27871.
XX
PR 06-OCT-1999; 99US-0413285.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Fuller MT, Hales KG, Santel AH;
XX
DR WPI; 2001-300165/31.
XX
PT New nucleic acid molecules encoding mitofusin polypeptides useful for
PT identifying anti-insect, antifungal and therapeutic agents -
XX
PS Example 12; Page 51; 92pp; English.
XX
CC The sequences given in AAB47231-45 represent the consensus sequences
CC and homologs from the GTPase domains from some mitofusin proteins.
CC Mitofusins are large predicted GTPases with a predicted transmembrane
CC domain, coiled-coil region and a C-terminal region showing a high
CC isoelectric point and a predicted coiled-coil region. They are
CC the first known protein mediators of mitochondrial fusion, e.g.
CC mediating developmentally regulated post-meiotic fusion of mitochondria
CC in Drosophila spermatids. Mitofusin polypeptides are useful for
CC enhancing membrane fusion in a population of membrane-bounded entities,
CC e.g., mitochondria. Mitofusin proteins are useful for screening
CC anti-insect or antifungal agent. Modulators of mitochondrial fusion
CC are useful for reducing fertility and increasing the mortality rate
CC of arthropod pest, e.g., an insect (claimed). Mitofusin DNA is
CC useful for generating genetically modified non-human animals or
CC site-specific gene modifications in cell lines, for the study of

```
CC   mitofusin function or regulation, and to create animal models of
CC   diseases, including mitochondrial diseases, muscle myopathies,
CC   neurodegenerative disorders, and aging. Mitofusins, and the DNA
CC   encoding them, can be used in assays to identify therapeutic agents
CC   useful for treating chronic neurodegenerative diseases such as
CC   Alzheimer's disease and Parkinsonian's disease, autoimmune diseases,
CC   diabetes mellitus, congenital muscular dystrophy with mitochondrial
CC   structural abnormalities, fatal infantile myopathy, mitochondrial
CC   encephalopathy, lactic acidosis, stroke, mitochondrial diabetes,
CC   deafness, neuropathy, progressive external ophthalmoplegia, optic
CC   atrophy, Leigh's syndrome, dystonia, stroke, schizophrenia, progressive
CC   joint disorders such as osteoarthritis, and hyperproliferative
CC   disorders such as cancer, tumour and psoriasis.
XX
SQ   Sequence   19 AA;

  Query Match             26.3%;  Score 5;  DB 22;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

      11 GRTSS 15
         |||||
Db       7 GRTSS 11


RESULT 18
AAR37218
ID   AAR37218 standard; peptide; 10 AA.
XX
AC   AAR37218;
XX
DT   06-SEP-1993  (first entry)
XX
DE   IL-6 antagonist peptide #2.
XX
KW   IL-6; antagonist; cytokine; B cell differentiation; inflammation;
KW   tissue injury; B9.9 hybridoma cell line; Castleman's Disease;
KW   Lennart's T-cell lymphoma; Non-Hodgkin's lymphoma; allergy;
KW   immune deficiency disease; cardiac myxoma;
KW   mesangial proliferative glomerulonephritis.
XX
PN   US5210075-A.
XX
PD   11-MAY-1993.
XX
PF   16-FEB-1990;   90US-0480868.
XX
PR   16-FEB-1990;   90US-0480868.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
PI   Chiang S,  Lobl TJ,  Nagarajan G,  Scholz W;
XX
DR   WPI; 1993-166970/20.
XX
PT   New peptide interleukin-6 antagonists - for treating and
PT   preventing auto-immune, immuno:inflammatory, neoplastic and
PT   infectious diseases etc.
XX
PS   Claim 9; Column 27; 20pp; English.
XX
CC   This peptide is a specifically claimed example of a highly generic
CC   formula covering sequences derived from the p51-70 portion (i.e the
CC   IL-6 receptor-binding portion) of IL-6 (see AAR37216) or modelled
CC   after different portions of this sequence. In an assay to determine
CC   IL-6 antagonist activity of this peptide, proliferation of the IL-6
CC   dependent B9.9 hybridoma cell line (J.Immunol. 139: 4116, 1987) was
CC   inhibited by 78 (+/-9)%.
CC   See AAR37216-R37261.
XX
SQ   Sequence   10 AA;

  Query Match             21.1%;  Score 4;  DB 14;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 SSKE 17
           ||||
Db       2 SSKE 5


RESULT 19
AAR63388
ID   AAR63388 standard; Protein; 10 AA.
XX
AC   AAR63388;
XX
DT   18-AUG-1995  (first entry)
XX
DE   Hepatitis C virus core protein polypeptide (variable region).
XX
KW   Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
KW   classification; immunisation; prophylaxis; serotyping.
XX
OS   Hepatitis C virus.
XX
PN   WO9425601-A.
XX
PD   10-NOV-1994.
XX
PF   27-APR-1994;   94WO-EP01323.
XX
PR   27-APR-1993;   93EP-0401099.
PR   05-AUG-1993;   93EP-0402019.
XX
PA   (INNO-) INNOGENETICS NV SA.
XX
PI   Maertens G,  Stuyver L;
XX
DR   WPI; 1994-358277/44.
XX
PT   New polynucleotide sequences from hepatitis C virus - and related
PT   vectors, polypeptide(s) and antibodies, useful for immunisation,
PT   treatment, diagnosis and typing of HCV isolates
XX
PS   Claim 15; Page 272; 404pp; English.
XX
CC   Compositions comprising at least 5, and pref. 8 or more contiguous
CC   nucleotides selected from an HCV type 3 genomic sequence, more
CC   particularly (i) the region spanning positions 417-957 of the
CC   Core/E1 region of HCV subtype 3a; (ii) the region spanning positions
CC   4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning
CC   positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the
CC   region spanning positions 8023-8235 of the NS5 region of the BR36
CC   subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic
CC   sequence, may be used as primers to amplify nucleic acid from an
CC   isolate belonging to a specific genotype, or as a probe for specific
CC   detection/classification of nucleic acid.  Polypeptides encoded by
CC   the nucleotides in such compositions may be used for immunisation
CC   against HCV, for the detection of antibodies directed against HCV
CC   and for serotyping.  The variable region in the core protein
CC   (V-CORE) of HCV has been shown to be useful for serotyping.
XX
SQ   Sequence   10 AA;

  Query Match             21.1%;  Score 4;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 GRTS 14
           ||||
Db       4 GRTS 7


RESULT 20
AAR63389
```

ID AAR63389 standard; Protein; 10 AA.
XX
AC AAR63389;
XX
DT 18-AUG-1995 (first entry)
XX
DE Hepatitis C virus core protein polypeptide (variable region).
XX
KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
KW classification; immunisation; prophylaxis; serotyping.
XX
OS Hepatitis C virus.
XX
PN WO9425601-A.
XX
PD 10-NOV-1994.
XX
PF 27-APR-1994; 94WO-EP01323.
XX
[redacted] 27-APR-1993; 93EP-0401099.
[redacted] 05-AUG-1993; 93EP-0402019.
XX
PA (INNO-) INNOGENETICS NV SA.
XX
PI Maertens G, Stuyver L;
XX
DR WPI; 1994-358277/44.
XX
PT New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates
XX
PS Claim 15; Page 272; 404pp; English.
XX
CC Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the
CC Core/E1 region of HCV subtype 3a; (ii) the region spanning positions
CC 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning
CC positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the
CC region spanning positions 8023-8235 of the NS5 region of the BR36
CC subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic
CC sequence, may be used as primers to amplify nucleic acid from an
CC isolate belonging to a specific genotype, or as a probe for specific
CC detection/classification of nucleic acid. Polypeptides encoded by
CC the nucleotides in such compositions may be used for immunisation
CC against HCV, for the detection of antibodies directed against HCV
CC and for serotyping. The variable region in the core protein
[redacted] (V-CORE) of HCV has been shown to be useful for serotyping.
XX
SQ Sequence 10 AA;

Query Match 21.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GRTS 14
|||| 
Db 4 GRTS 7

RESULT 21
AAW21262
ID AAW21262 standard; peptide; 10 AA.
XX
AC AAW21262;
XX
DT 29-JUL-1997 (first entry)
XX
DE Hydroxymethylglutaryl coenzyme A reductase signal oligopeptide #21.
XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US00575.
XX
PR 14-JAN-1994; 94US-0182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication
PT between protein(s)
XX
PS Claim 5; Page 33; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface
CC of the protein and are represented by the hydrophilicity maxima of
CC the protein. These peptides are enriched in charged amino acids
CC arranged with neutral spacer amino acids. The specific signal
CC character of these oligopeptides is determined by a characteristic
CC combination of conformation and charge within the signal sequence.
CC These oligopeptides may be used as vaccines in the treatment of
CC human disease, as competitive inhibitors to prevent or reduce the
CC metabolic action or interaction of a selected protein by blocking
CC its specific signal sequences, or as therapeutic agents to function
CC as feedback regulators to reduce synthesis rate of a selected protein.
CC These peptides may be modified by omitting one or more amino acids at
CC the N- and/or C-terminal, by substituting one or more amino acids
CC without consideration of charge and polarity, by substituting one or
CC more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
XX
SQ Sequence 10 AA;

Query Match 21.1%; Score 4; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SSKE 17
|||| 
Db 3 SSKE 6

RESULT 22
AAW12579
ID AAW12579 standard; peptide; 10 AA.
XX
AC AAW12579;
XX
DT 08-APR-1997 (first entry)
XX
DE SH2 binding peptide #9.
XX
KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;

```
KW   signal transduction pathway; non-insulin dependent diabetes;
KW   insulin-resistant diabetes.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /label= OTHER
FT                   /note= "opt. selected from tyrosine, phosphotyrosine,
FT                          tyrosine isosteres, and phosphotyrosine
FT                          isosteres"
XX
PN   WO9623813-A1.
XX
PD   08-AUG-1996.
XX
PF   31-JAN-1996;   96WO-US01544.
XX
PR   01-FEB-1995;   95US-0382100.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Gordeev MF,  Gordon E,  Grove JR,  Hart CP,  Kim MH;
PI   Patel DV,  Szardenings AK;
XX
DR   WPI; 1996-371373/37.
XX
PT   Peptide(s) which bind to SH2 domains - are used to treat diseases
PT   associated with aberrant cell growth, differentiation or regulation
PT   associated with defects in receptor tyrosine kinase pathways
XX
PS   Claim 14; Page 118; 203pp; English.
XX
CC   The sequences given in AAW12571-614 represent src homology region 2
CC   (SH2) binding peptides which contain a core peptide which corresponds to
CC   the formula:
CC                   Z7-X-Z8-X
CC   X = any D- or L- amino acid;
CC   Z7 = phosphotyrosine or its isostere;
CC   Z8 = asparagine or its isostere;
CC   the amino terminus is acylated, and the peptide is less than 14
CC   residues in length, with the proviso that if Z7 is phosphotyrosine
CC   and Z8 is asparagine, then the peptide is not GDGZ7XZ8XPLLL.
CC   These SH2 binding peptides are used to treat of diagnose diseases
CC   associated with aberrant cell growth, differentiation or regulation
CC   which is associated with defects in receptor tyrosine kinase pathways,
CC   by partially blocking or inhibiting a cellular signal transduction
CC   pathway.  The disease may be cancer, a developmental or differentiation
CC   disease or insulin-resistant (or non-insulin dependent) diabetes.
XX
SQ   Sequence   10 AA;

  Query Match             21.1%;  Score 4;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 NVPG 4
           ||||
Db       6 NVPG 9


RESULT 23
AAW12570
ID   AAW12570 standard; peptide; 10 AA.
XX
AC   AAW12570;
XX
DT   08-APR-1997  (first entry)
XX
DE   SH2 binding peptide core sequence #20.
XX
KW   Core peptide; src homology region 2 binding peptide; SH2; cell growth;
KW   differentiation; regulation; receptor tyrosine kinase pathway; cancer;
KW   signal transduction pathway; non-insulin dependent diabetes;
KW   insulin-resistant diabetes.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /label= OTHER
FT                   /note= "opt. phosphotyrosine"
XX
PN   WO9623813-A1.
XX
PD   08-AUG-1996.
XX
PF   31-JAN-1996;   96WO-US01544.
XX
PR   01-FEB-1995;   95US-0382100.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Gordeev MF,  Gordon E,  Grove JR,  Hart CP,  Kim MH;
PI   Patel DV,  Szardenings AK;
XX
DR   WPI; 1996-371373/37.
XX
PT   Peptide(s) which bind to SH2 domains - are used to treat diseases
PT   associated with aberrant cell growth, differentiation or regulation
PT   associated with defects in receptor tyrosine kinase pathways
XX
PS   Claim 8 and 13; Page 116-117; 203pp; English.
XX
CC   The sequences given in AAW12551-70 represent core peptides of an src
CC   homology region 2 (SH2) binding peptide which correspond to the
CC   formula:
CC                   Z7-X-Z8-X
CC   X = any D- or L- amino acid;
CC   Z7 = phosphotyrosine or its isostere;
CC   Z8 = asparagine or its isostere;
CC   the amino terminus is acylated, and the peptide is less than 14
CC   residues in length, with the proviso that if Z7 is phosphotyrosine
CC   and Z8 is asparagine, then the peptide is not GDGZ7XZ8XPLLL.  SH2
CC   binding peptides containing these core peptides are used to treat of
CC   diagnose diseases associated with aberrant cell growth, differentiation
CC   or regulation which is associated with defects in receptor tyrosine
CC   kinase pathways, by partially blocking or inhibiting a cellular signal
CC   transduction pathway.  The disease may be cancer, a developmental or
CC   differentiation disease or insulin-resistant (or non-insulin dependent)
CC   diabetes.
XX
SQ   Sequence   10 AA;

  Query Match             21.1%;  Score 4;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 NVPG 4
           ||||
Db       6 NVPG 9


RESULT 24
AAY55308
ID   AAY55308 standard; peptide; 10 AA.
XX
AC   AAY55308;
XX
DT   07-JAN-2000  (first entry)
XX
DE   CD34 antigen antigenic peak peptide SEQ ID NO:202.
XX
KW   Antibody releasing peptide; CD34; hybridoma; binding; antigen;
KW   cell surface antigen; identification; haematopoietic stem cell;
KW   tumour; cancer; immune system; therapy; displacement.
```

XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5968753-A.
XX
PD 19-OCT-1999.
XX
PF 07-JUN-1995; 95US-0482228.
XX
PR 14-JUN-1994; 94US-0259427.
XX
PA (NEXE-) NEXELL THERAPEUTICS INC.
XX
PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
PI Al-Abdaly FA;
XX
DR WPI; 1999-590399/50.
XX
Short peptides useful for displacing antibodies from cell surface
antigens. -
XX
PS Example 11; Column 38; 81pp; English.
XX
CC The present invention describes peptides of 4-17 amino acids which
CC displace either the anti-CD34 monoclonal antibody designated 561, the
CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC
CC HB-11646 (designated 9069), the anti-CD34 antibody produced by
CC hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer
CC antibody produced by hybridoma ATCC HB-11884 (9187), from a cell
CC surface antigen on a target cell. The peptides are useful for
CC displacing antibodies bound to cell surfaces to release cells that
CC have been positively selected by antibody-mediated binding to beads
CC or other solid support. AAY55107 to AAY55319 represent peptides used in
CC the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 21.1%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TSSK 16
||||
Db 6 TSSK 9

SULT 25
06153
AAY06153 standard; Peptide; 10 AA.
XX
AC AAY06153;
XX
DT 16-AUG-1999 (first entry)
XX
DE scFv 9A4 clone 23A VH CDR3 region.
XX
KW Type II collagen; assay; antibody; rheumatoid arthritis;
KW osteoarthritis; diagnosis; monoclonal antibody; MAb; scFv;
KW single chain antibody; complementarity determining region; CDR;
KW mutant.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "Ala in native sequence"
FT Misc-difference 5
FT /note= "Gly in native sequence"
FT Misc-difference 10
FT /note= "unidentified residue"
XX
PN EP921395-A2.
XX
PD 09-JUN-1999.
XX
PF 12-NOV-1998; 98EP-0309266.
XX
PR 13-NOV-1997; 97US-0065423.
XX
PA (PFIZ ) PFIZER PROD INC.
XX
PI Downs JT, Johnson KS, Mezes PS, Otterness IG;
XX
DR WPI; 1999-315488/27.
XX
PT Monitoring biological media for collagen fragments, using capture
PT and/or detection antibodies
XX
PS Example 8; Page 30; 64pp; English.
XX
CC This sequence represents the mutated complementarity determining
CC region CDR3 of the heavy chain variable region (VH) of single chain
CC antibody scFv 9A4 clone 23A. It has 2 amino acid changes from the
CC parent 9A4 VH CDR3 clone (see AAY06150). A library of 9A4 scFvs was
CC expressed in E. coli that carried mutated CDR3 sequences (see
CC AAY06151-81). Binding studies to a collagen fragment demonstrated
CC that changes could be made to the amino acid sequence of the parent
CC scFv (see also AAY06130) while still retaining binding to the target.
CC By altering different regions of 9A4 VH and VL, antibodies with
CC variable to enhanced binding properties relative to the parent
CC antibody can be produced. The invention provides a method for
CC monitoring biological media for collagen II fragments, using capture
CC and detection antibodies such as 9A4 and its engineered variants.
CC The method can be used to assess the breakdown of type II collagen
CC by collagenase in normal and pathological (rheumatoid arthritis,
CC osteoarthritis) conditions.
XX
SQ Sequence 10 AA;

Query Match 21.1%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GRGR 12
||||
Db 2 GRGR 5

Search completed: May 9, 2003, 16:05:27
Job time : 35 secs